

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 19:12:49 ; Search time 2247 Seconds  
(without alignments)  
5426.840 Million cell updates/sec

Title: US-09-830-228-51

Perfect score: 2487

Sequence: 1 ATTATTATACAGAAACCTCT.....TTAAGACACTTTGAAGAAGA 2487

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
  - 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
  - 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
  - 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
  - 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
  - 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
  - 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
  - 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
  - 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
  - 13: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
  - 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
  - 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
  - 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
  - 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
  - 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
  - 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	229.6	9.2	1300	17	US-10-668-749A-1
2	175.6	7.1	6668	15	Sequence 1, Appli
3	167	6.7	1204	17	Sequence 1670, Ap
4	161.2	6.5	6292	13	Sequence 77858, A
5	157	6.3	803	17	Sequence 461, App
6	154.2	6.2	14006	15	Sequence 72176, A
7	154	6.2	627	17	Sequence 1931, Ap
8	152.8	6.1	3673778	15	Sequence 9336, Ap
9	150.2	6.0	7442	13	Sequence 2, Appli
10	148.2	6.0	2520	17	Sequence 409, App
11	147	5.9	6767	13	Sequence 205, App
12	144.2	5.8	9539	15	Sequence 330, App
13	144.2	5.8	9539	15	Sequence 52, Appl
14	144	5.8	6334	15	Sequence 54, Appl
					Sequence 1186, Ap

C 15	141.2	5.7	34769	13	US-10-221-714A-501	Sequence 501, App
C 16	141	5.7	8079	17	US-10-240-589C-122	Sequence 122, App
C 17	140.4	5.6	31124	13	US-10-087-192-463	Sequence 463, App
C 18	139.8	5.6	529	9	US-09-983-965-2103	Sequence 2109, Ap
C 19	138.8	5.6	16033	15	US-10-311-455-1377	Sequence 1377, Ap
C 20	138.6	5.6	868	17	US-10-437-963-42302	Sequence 42302, A
C 21	137.8	5.5	9964	15	US-10-311-455-71	Sequence 71, Appl
C 22	136.4	5.5	3673778	15	US-10-312-841-1	Sequence 1, Appli
C 23	135	5.4	1214	13	US-10-424-599-102083	Sequence 102083,
C 24	134.4	5.4	5493	13	US-10-221-613-349	Sequence 349, App
C 25	133.2	5.4	7571	15	US-10-311-455-500	Sequence 500, App
C 26	132.8	5.3	522	14	US-10-101-487-71	Sequence 71, Appl
C 27	132.8	5.3	530	14	US-10-101-487-73	Sequence 69, Appl
C 28	132.8	5.3	554	14	US-10-101-487-69	Sequence 106, App
C 29	132.8	5.3	554	14	US-10-101-487-106	Sequence 1692, Ap
C 30	132.6	5.3	17934	15	US-10-311-455-1692	Sequence 9573, Ap
C 31	132	5.3	447	17	US-10-021-323-9573	Sequence 204, App
C 32	131.6	5.3	3505	17	US-10-389-566-204	Sequence 240, App
C 33	131.2	5.3	6419	15	US-10-311-455-240	Sequence 3400, Ap
C 34	130	5.2	446	9	US-09-960-352-3400	Sequence 157, App
C 35	129.6	5.2	15387	15	US-10-311-455-157	Sequence 1669, Ap
C 36	129.2	5.2	6668	15	US-10-311-455-1669	Sequence 70401, A
C 37	127	5.1	767	13	US-10-424-599-70401	Sequence 109362,
C 38	125.8	5.1	712	13	US-10-021-323-4874	Sequence 4874, Ap
C 39	125.2	5.0	508	17	US-10-311-455-945	Sequence 945, App
C 40	124.8	5.0	6145	15	US-10-311-455-2147	Sequence 2147, Ap
C 41	124	5.0	113515	15	US-10-282-122A-16542	Sequence 16542, A
C 42	123.4	5.0	1533	13	US-10-021-323-10810	Sequence 10810, A
C 43	123.2	5.0	529	17	US-10-311-455-761	Sequence 761, App
C 44	123	4.9	6171	15	US-10-239-676-51	Sequence 51, Appl
C 45	123	4.9	9539	15		

ALIGNMENTS

RESULT 1  
US-10-668-749A-1  
; Sequence 1, Application US/10668749A  
; Publication No. US20040110205A1  
; GENERAL INFORMATION:  
; APPLICANT: Agilent Technologies  
; TITLE OF INVENTION: Methods and Systems for Nanopore Data Analysis  
; FILE REFERENCE: 50112-1580  
; CURRENT APPLICATION NUMBER: US/10/668,749A  
; CURRENT FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1300  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-668-749A-1

Query Match	9.2%	Score 229.6;	DB 17;	Length 1300;
Best Local Similarity	48.6%	Pred No. 7,2e+23;		
Matches	625;	Conservative	0;	Mismatches 661; Indels 0; Gaps 0;
QY	1152	AAAGATGCAACTGGTATAAATTCAGAACAAATATATAAAGGAAAGTTCAAGGATTTTA	1211	
Db	1	AA	60	
QY	1212	GAAAGATTTTAGATCCAGTAAGGATAAATTTGTTCCAAATGTCCTAATGACAGATGAA	1271	
Db	61	AA	120	
QY	1272	TTGGCAAAATAATTCAAGAGAGAAAGAGTAAATAACGGGGAGAGAGAAATGATATAA	1331	
Db	121	AA	180	
QY	1332	GCTGCTCTTTTAGGAGAGATCAAAAGAGAGTGAAGAGAGAAATGAGCAGCTGTTAT	1391	





Query Match	6.3%	Score 157;	DB 17;	Length 803;
Best Local Similarity	51.8%;	Pred. No. 8.5e-13;		
Matches 310;	Conservative 0;	Mismatches 288;	Indels 0;	Gaps 0;
Qy	1137	AAAGATGCAACTGGTAAAGATGCAACTGCTAAATATGACAGACAAATATATAAAGCGAAA	1196	
Db	798	AANNGANAATAAGANAAAAAATAAAGAAAAAAGAAAAAANAAAAAAGANAGAAAAA	739	
Qy	1197	GTTCAAGGATTTTGAAGAAAGATTTTAGATCCAGTAAAGGATAAAATGCTTCAAAATGTT	1256	
Db	738	AAAAAAGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA	679	
Qy	1257	CCAAATAGCAGATGAATGTCGAAAAAAATTTACAAGAGAGAAAAAGCTGAATACGGGGAA	1316	
Db	678	GAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA	619	
Qy	1317	GAGGAAAAATGATAAAGCTCTCTTTTAGCAGAGAGATCAAAAGAGGATGAAGAGAAAAAT	1376	
Db	618	AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA	559	



Qy	1377	GAGCAAGCTGTTAAATTTAGAGAAAAAATTCGCGAAGAGAGATAGAAGTTGTGTAATTTA	1436
Db	558	AGAAAAAGAAAAAATAA	499
Qy	1437	GAAGAGAAAGAAATTTAGAGAGTTTAAAAAAGAGACTGAAGAGATGAAGAGATAAAGAGAAATA	1496
Db	498	AAAAAATAAAAAAAAAAAGAAAAAATAAAAAAAAAAAGAAAGAAAAAATAAAAAAAAAA	439
Qy	1497	GAGNAACAAAAACAGAGAGTTGGAAAAAGCACAGAAAGAAAAACAACGACAGAGAAAG	1556
Db	438	AGAAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAA	379
Qy	1557	AAACGAAAAAATAACAGAAACGACAGAGAGAAAAAGAAACGAAACGCAAGAACCAAGAAAA	1616
Db	378	AAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAA	319
Qy	1617	GAGAGAGAGCTTAAACACAAATTTAAAAAACTTCGCGNTAAATAGATAGATAAGTTGG	1676
Db	318	AAAGAAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAAATAAAAAAAAAA	259
Qy	1677	AATATTGATGGTATAGAAAGTCAAACAAAGTGTAAAAACCGAAAGCAGTTATAGATAAAA	1734
Db	258	AAGAGACGAGAAAAAGCAAGAAAAAATAAAAAAGAAAGANNAGNNAGNNNNNAGAGAAA	201

RESULT 6  
US-10-311-455-1931/c  
; Sequence 1931, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: CLEX, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Expression of Specific Genes

```

? TITLE OF INVENTION: Diagnosis of diseases associated with the immune system of
? FILE REFERENCE: 5013.1014
? CURRENT APPLICATION NUMBER: US/10/311.455
? CURRENT FILING DATE: 2002-12-16
? PRIOR APPLICATION NUMBER: PCT/EP01/07537
? PRIOR FILING DATE: 2001-07-02
? PRIOR APPLICATION NUMBER: DE 10032529.7
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: DE 10043826.1
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ ID NOS: 2424
? SEQ ID NO 1931
? LENGTH: 14006
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: 8289, 8310, 8313
? OTHER INFORMATION: n is a or g or c or t
? US-10-311-455-1931

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	Query Match	6.2%;	Score 154.2;	DB 15;	Length 14006;
	Best Local Similarity	53.6%;	Pred. No. 5.2e-12;		
	Matches 321;	Conservative	0;	Mismatches 278;	Indels 0; Gaps 0;
Qy	1136	TAAAGATCCAACTGGTAAAGATGCAACTGGTAAAAATCGACGACAAATATATAAAGGAA			1195
Db	2500	TATACATATATAA			2441
Qy	1196	AGTTCAAGGATTTTGTAGAAAAAGATTTTGTAGTCCAGTAAAGGATAAAAATTTGCTTCAAAATGG			1255
Db	2440	AAA			2381
Qy	1256	TCCAATACAGATGAATTTGGCAAAAAAAATTTCAAGACGACGAAAGGTAAATATACGGGGA			1315
Db	2380	CCAATATAATATAAAAAA			2321

Qy	1316	AGAAGAAAATGATAAAAGCTGCTCTTTTAGCGAGAGATCAAAAGAGAGTGAAGAGAGAAA	1375
Db	2320	AAAAAAAAAAAAAAAAAACCAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAT	22615
Qy	1376	TGACCAAGCTGTTAAATTTCAGAGAGAAAAAATTCGCAAGAGGATGAAGAAAGTTGTTAATTT	14355
Db	2360	AAAAAAAAAAAAAAAAACGAAAAAATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAT	22015
Qy	1436	AGAAGAGAAAGAAATTAGAAGCTTAAAAAGAGAGCTGAAGAGACATGAAGATTAAGAGAGAAAT	14955
Db	2200	AATTCAAAAAAA	21415
Qy	1496	AGAGAAACAAACCAAGAGTGGHAAAAAGCAGAGAAAGHAAACACGACAGAGAGAGAAA	15555
Db	2140	AATTAATAAAAAAAAAAAAAAAAAAAA	20815
Qy	1556	GAAACGAAAAAAACCAAGACAGCAAGAGAGAAAAAGAAAAAGAAAAACGACAGAGAACAAAGAAA	16155
Db	2080	AAAAAAAAAATTAATAA	20215
Qy	1616	AGAAAGGAGAGCTAAAAACAAAAATTAATAAAACCTTCGCGATAAAAATAGATGAGATAAGTTG	16755
Db	2020	AAAAAAAAAAAAATCAAATAA	19615
Qy	1676	GAATATTGATGGTATAGAAAGCTCAACCAAGTGTTAACCCGAAACGAGCTTTATAGATAAAA	1734
Db	1960	AATAAAAAAAAAAAAAAAAAA	1902

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RESULT 7
US-10-021-323-9336
; Sequence 9336, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Peng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 9336
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-024-Q6-K6-C2
US-10-021-323-9336

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Query Match	6.2%	Score 154;	DB 17;	Length 627;
Best Local Similarity	52.9%;	Pred. No. 2.1e-12;		
Matches 331;	Conservative 0;	Mismatches 295;	Indels 0;	Gaps 0
QY	1369	AAGAAAATGACCAAGCTGTTTAATTTAGAAGAAAAAAATGCGGAAGAGGATGAAGAAGTTG	1429	
Db	2	AAGGAAAAAA	61	
QY	1429	TTAATTTTGAAGAGAAAGAAATTTAGAGTGTAAAAAAGAGACTGAAGAAGATGAAGATAAAG	1489	
Db	62	AGAAAAAATAAAAAAAAAAAAAAAAAAGGAAAAAATAAGAAAAAATAAAAAA	121	
QY	1489	AAGAAATGAGAAACAAAAACAAGATGCGAAAAAGCACAGAAAGAAACAACGACAAAG	1549	
Db	122	AAAAAAAAAAAAAGGAAAAAGAAAAAAGAAAAAATAAAAAAATAAGAAAAAATAAGAAAAA	181	
QY	1549	AAGAAAAAGAAACGAAAAAATAAAGAACGACAAAGAAAGAAAAAGAAACGAAACGACAAAGAC	1609	

Db 182 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAGAAAAAAAAAAAAAAAAAAAAAAAAA 241  
Qy 1609 AAAGAAAAGAGAGAGCTAAACCAAAATTAATAAATTCGCGATATAATAGATGAGA 1668  
Db 242 AAGGAAAAAAAAAGAAA 301  
Qy 1669 TAAGTTGGAATATTGATGGTATAGAAAGTCAACAGAGTGAACCGAAGCAGTATTAG 1728  
Db 302 GAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 361  
Qy 1729 ATAAATTTACGGGCTGTATATGATTATTTTACCGATGACACAAAGAGCTATATATA 1788  
Db 362 AA 421  
Qy 1789 AAACATCGGAGATTTTGAAGAGTGAAGAGCGAGGATTTGGAAATTTATTGAAAGAAAT 1848  
Db 422 AAAAAAAAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 481  
Qy 1849 TGAGTGATCTAGAGTGAAGTGAAGACCAATTAATTAAGATATAATTAATTAATG 1908  
Db 482 AAAAAAAAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 541  
Qy 1909 CCCATGAAATGAGCTCTCTTAAAGAAATGTAGATGTCAGCGAAATTTAAAGAAAGATT 1968  
Db 542 AAAAAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 601  
Qy 1969 TAGAAGATTAATCATCGGATTTAGAA 1994  
Db 602 AAGGAAAAAAAAAGAGAGAGAGAA 627

RESULT 8  
US-10-312-841-2/c  
; Sequence 2, Application US/10312841  
; Publication No. US20030186277A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
; FILE REFERENCE: E01/1208/WO  
; CURRENT APPLICATION NUMBER: US/10/312,841  
; PENDING FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 3673778  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; NAME/KEY: unsure  
; LOCATION: (379615)  
US-10-312-841-2

Query Match  
Best Local Similarity 6.1%; Score 152.8; DB 15; Length 3673778;  
Matches 343; Conservative 0; Mismatches 317; Indels 0; Gaps 0;  
Qy 1068 TTTGTGCTGATAAGTTCTTGCAAGATTTGATGCAACTGGTAAAGATGCAACTGGTAAAGAT 1127  
Db 972186 TTTATTTTATTTTATTTTATTTTATCAATTAATTAATTAATTAATTAATTAATCA 972127  
Qy 1128 GCACTGGTAAAGATGCACTGGTAAAGATGCACTGGTAAAGATGCACTGGTAAAGATTA 1187  
Db 972126 ACTACTTAAAGATGCACTGGTAAAGATGCACTGGTAAAGATGCACTGGTAAAGATTA 972067  
Qy 1188 AAAGGAAAGTTCAAGGATTTTGAAGAAAGATTTTGAAGTCCAGTAAAGATTAATTTGCT 1247  
Db 972066 ACCACTACACTTCAACTATCAACAAACAAATCTATCTCCAAACAAACAAACAAACAA 972007  
Qy 1248 TCAATTTGTTCAATAGCAGATGATTTGGCAAAAGAAATTTCAAGAGAGAGAAAGTAAAT 1307  
Db 972006 AA 971947

Qy 1308 AACGGGGAAGAGAAATGATAAAGCTGCTCTTTTAGGAGAGAAATCAAAAGAGGATGAA 1367  
Db 971946 AAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 971887  
Qy 1368 GAAGAAATAGCAAGCTGTTTAAATTTAGNAGAAAGAAATGCGGAGAGGATAGAAAGTT 1427  
Db 971886 AA 971827  
Qy 1428 GTTATTTTAGAAGAGAAAGATTTAGAAGTTTAAAAAGAGAGCTGAAGAGATGAAGATAA 1487  
Db 971826 AA 971767  
Qy 1488 GAAGAAATAGAGAAACAAACAAACAAAGAGTGGAAAGCAAGAAAGAAACCAACGCA 1547  
Db 971766 AA 971707  
Qy 1548 GAAGAAAGAAAGCAAGAAAGAAAGCAAGAGAGAGAAAGAAAGCAAGAAAGCAAGAA 1607  
Db 971706 AA 971647  
Qy 1608 CAAGAAAGAAAGAGAGAGCTTAAACAAATTTAAAAAATTCGCGATTAATAATAGATGAG 1667  
Db 971646 AA 971587  
Qy 1668 ATAAGTTGAGATTTGATGCTATAGAAAGTCAACACAGTGTAAACCGAAGCAGTTATA 1727  
Db 971586 AA 971527

RESULT 9  
US-10-221-714A-409/c  
; Sequence 409, Application US/10221714A  
; Publication No. US20040048254A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with  
; FILE REFERENCE: 5013.1005  
; CURRENT APPLICATION NUMBER: US/10/221,714A  
; PENDING FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: PCT/BP01/02955  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: DE 10013847.0  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 540  
; SEQ ID NO 409  
; LENGTH: 7442  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; NAME/KEY: unsure  
; LOCATION: 1792, 4861..4862  
; OTHER INFORMATION: n is a or g or c or t  
US-10-221-714A-409

Query Match  
Best Local Similarity 6.0%; Score 150.2; DB 13; Length 7442;  
Matches 446; Conservative 0; Mismatches 468; Indels 5; Gaps 1;  
Qy 1213 AAAAGATTTTAGATCCAGTAAAGGATAAAATTCCTTCAATGTCCTCAATAGCAGATGAAT 1272







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; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1186
; LENGTH: 6334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1186

Query Match      5.8%; Score 144; DB 15; Length 6334;
Best Local Similarity 49.5%; Pred. No. 1.1e-10;
Matches 400; Conservative 0; Mismatches 405; Indels 3; Gaps 1;

Qy 1259 AATGACGATGAATGGCAAAAATAATACAGAAGAGAAAGGTAAATAACGGGGAAGA 1318
Dy 1221 AAAAATCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1162
Qy 1319 AGAAATGATAAGCTGCTTTTAGGAGAGAGATCAAAAGAGGATGAAGAGAAATGA 1378
Dy 1161 AACCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1102
Qy 1379 GCAAGCTGTTAATTAGAGAAAAAATGCGAAGAGGATGAAGAGAGTGTGTTAATTGA 1438
Dy 1101 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1042
Qy 1439 AGAGAGAGATTAAGAGTTAAATAAAGAGACTGAAGAGATGAAGATGAAGAGAAATGA 1498
Dy 1041 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 982
Qy 1499 GAAACAAAAACAAGAGTGGAAAAAGCACAAGAAAGAAAAACACGACAAAGAAAGAA 1558
Dy 981 AAAAAACCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 922
Qy 1559 ACGAAAAAACAAGACAGACAGAGAGAAAGAAACGAAACGACAGAAACAAAGAAAGA 1618
Dy 921 AACCGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 862
Qy 1619 AAGGAGAGCTAAAAACAATAATTAATAAATAAATAAATAAATAAATAAATAAATAA 1678
Dy 861 CGCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 802
Qy 1679 TATTGATGATAGAAAGTCAAAACAAGTGTAAACCGAAAGCGAGTTATAGATTAATA 1738
Dy 801 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 742
Qy 1739 GGGGCTGTATGATTTATTTACCGATGACACAAAAAGCTATATATATAAACAATGGG 1798
Dy 741 AACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 682
Qy 1799 AGATTTAGAGATGAAGAGCGGAGAGATTTGGAAAAATTTATTGAAAGATTTGAGTGAT 1858
Dy 681 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 622
Qy 1859 TAGAGATGAGTTAAGAACCAATTAATAAAGTAAATAAATAAATAAATAAATAAATAA 1918
Dy 621 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 562
Qy 1919 TGAGCTCTCTTAAAAAGAAATGTAGATGTCAGCGAAATTTAAAGAGATTTTAAAGAA 1978
Dy 561 AAAAACTCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 505
Qy 1979 AATAATCAGGATTGAAGAGTTAAGAAATATCTTAAAGCAATTTCTAATTTGAAGAAAT 2038
Dy 504 AAAAAACCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 445
Qy 2039 TAAAGGATACATCAGTTACAGTCAGTAA 2066
Dy 444 AACGCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 417

RESULT 15
US-10-221-714A-501/c
; Sequence 501, Application US/10221714A

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; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221.714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 501
; LENGTH: 34769
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-501

Query Match      5.7%; Score 141.2; DB 13; Length 34769;
Best Local Similarity 49.7%; Pred. No. 4.5e-10;
Matches 386; Conservative 0; Mismatches 388; Indels 2; Gaps 1;

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Job time : 2267 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 16:02:38 ; Search time 6240 Seconds  
(without alignments)  
11901.802 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: em\_esthum:\*\*
- 3: em\_estin:\*\*
- 4: em\_estmu:\*\*
- 5: em\_estov:\*\*
- 6: em\_estpl:\*\*
- 7: em\_estro:\*\*
- 8: em\_hic:\*\*
- 9: gb\_est1:\*\*
- 10: gb\_est2:\*\*
- 11: gb\_hic:\*\*
- 12: gb\_est3:\*\*
- 13: gb\_est4:\*\*
- 14: gb\_est5:\*\*
- 15: em\_estfun:\*\*
- 16: em\_estom:\*\*
- 17: em\_gss\_hum:\*\*
- 18: em\_gss\_inv:\*\*
- 19: em\_gss\_pln:\*\*
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- 23: em\_gss\_mus:\*\*
- 24: em\_gss\_pro:\*\*
- 25: em\_gss\_rod:\*\*
- 26: em\_gss\_phg:\*\*
- 27: em\_gss\_vri:\*\*
- 28: gb\_gss1:\*\*
- 29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	232.8	9.4	1531	29	CG748014 P041-4-B0
C 3	226	9.1	1491	29	CG753221 P048-2-A0
C 4	223.4	9.0	1811	29	CG753732 P048-4-G0

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6	218.2	8.8	1313	29	CG751144	CG751144 P045-3-E0
7	214.8	8.6	1376	29	CG747831	CG747831 P041-3-B0
8	214.4	8.6	1596	28	CC293489	CC293489 CH261-62N
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14	209.6	8.4	1211	29	CG747324	CG747324 P040-4-D1
15	209.4	8.4	1377	29	CG749971	CG749971 P044-2-E0
16	209.2	8.4	1297	29	CG758143	CG758143 P053-3-B1
17	208.8	8.4	1324	29	CG746828	CG746828 P040-1-G1
18	207.8	8.4	1433	29	CG745119	CG745119 P037-4-G0
19	207.2	8.3	1389	29	CG747695	CG747695 P041-2-D0
20	207	8.3	1288	29	CG744915	CG744915 P037-3-F0
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ALIGNMENTS

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

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P053-1-D07.zc Pda EcoRI BAC Library Pristionchus pacificus genomic,  
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CG757757.1 GI:37986636  
GSS.  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 1566)  
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
22835951  
12884007  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071501371  
Fax: 00497071501498  
Email: raif.sommer@tuebingen.mpg.de

FEATURES		Class: BAC ends.		Location/Qualifiers	
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		Matches		584; Conservative 0; Mismatches 786; Indels 0; Gaps 0;	
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genomic survey sequence.  
ACCESSION  
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VERSION  
CG748014.1 GI:37968940  
KEYWORDS  
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SOURCE  
Pristionchus pacificus  
ORGANISM  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE  
1 (bases 1 to 1531)  
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
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Location/Qualifiers  
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VERSION  
CG753221.1 GI:37977480  
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE  
1 (bases 1 to 1491)  
AUTHORS  
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet.  
22835951  
PUBMED  
12884007  
COMMENT  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
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Location/Qualifiers  
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the genomic DNA with EcoRI and cloning into the BAC  
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Db 1370 ANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1311
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Db 830 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 771
Qy 1809 GATCAAGAGCGGAGATTTGGGAAATTTATTCGAAAGATTTGAGTGATCTAGAGATGAG 1868
Db 770 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 711
Qy 1869 TTAAGAACCAATTAATAAGATATAAAAAATATTATGCCCATGAAATGAGCTCT 1928
Db 710 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 651
Qy 1929 CTAAGAGAAATCTAGATGTCAGCGAAATTAAGAGAGATTTAGAAAACTAAATCAGGA 1988
Db 650 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 591
Qy 1989 TTGAAAAAGGTTAAGAGATATCTTAAGACAATTTCTAAATTTTCAAGAAATTTAAGGATAC 2048
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Qy 2049 ATCAGTTACAGTCAAGTAATTTATTTGATGCTCTTTAGATGTAATTTTACGTACAC 2108
Db 530 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 471
Qy 2109 AAAATACAGCTAGTAGAAAAAGTTCACTGGCTGTTATTTTTTTGTAGATTTTCATTTGTTAT 2168
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Db 410 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 351
Qy 2229 AATGTTGTTTATTTATATCTCTCTAGAGCTATGACGTATACAAATGAGATTTTCAAGATT 2288
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Qy 2289 TGATGATATTTATATAGAAACCAAAAGAAATAGATAAATCTTATTAACAGCTCTA 2348
Db 290 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 231
Qy 2349 TTTAACTAGCCNAATACTCTTAAAGCAAAAAAGACAAATNTACAGTCTCTTTGAAAGAA 2408
Db 230 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 171
Qy 2409 CAAAAATACGTAATAAAACCGGAGAAAA 2437
Db 170 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 142

RESULT 4
CG753732/c
LOCUS CG753732
DEFINITION P048-4-G03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION CG753732
VERSION CG753732.1 GI:37978509
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1811)
AUTHORS Srinivasan,J., Sin,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus
pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES
source
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match 9.0%; Score 223.4; DB 29; Length 1811;
Best Local Similarity 41.2%; Pred. No. 2e-18;
Matches 542; Conservative 0; Mismatches 770; Indels 2; Gaps 1;

Qy 1152 AAGATCCACTGGTAAAAATGCAGACAAAAATATAAGGGAAGTTCAAGATTTTA 1211
Db 1680 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1621
Qy 1212 GAAAGATTTTGTAGTCCGTAAGGATATAATTCGTTCAAATGCTCCAAATAGCAGATGAA 1271
Db 1620 NAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1561
Qy 1272 TTGCAAAAAATTCAGAGAGAGAAAGGTAAATACGGGGAAGAAATGATATAA 1331

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1560 AA 1501  
1332 GCTGCTTTTGGAGAGAAATCAAAAGAGGATGAAGAGAGAAATGAGCAAGCTGTAAT 1391  
1500 AA 1441  
1392 TTAGAGAGAAAAATCGGAGAGGATTAAGAAAGTTGTTAAATTTAGAGAGAAAGATTA 1451  
1440 AA 1381  
1452 GAAGTTTAAAAAGAGACTGAAGAGATGAAGATAAAGAGAGAAATAGAGAGAAACAA 1511  
1380 AA 1321  
1512 GAAGTGAAGAAACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1571  
1320 AA 1261  
1572 GAACAGCAAG 1629  
1260 AA 1201  
1630 AA 1689  
1200 AA 1141  
1690 TAGAAAGTCAACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1749  
1140 AA 1081  
1750 ATGATTATTTACGATGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1809  
1080 NAAA 1021  
1810 ATGAGAGAGCGAG 1869  
1020 AA 961  
1870 TAAGAACCAAAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1929  
960 AA 901  
1930 TAAAG 1989  
900 NAAA 841  
1990 TAGAAAGGTTAAGAGATATCTTAAAGACAAATCTTAAATTTGAAGAGAGATACA 2049  
840 AA 781  
2050 TCAGTTACAGTCAGTAAATTAATTTGGAGCTTTTGGAGTAACTAAATTTTACGACACA 2109  
780 NNNNNNAA 721  
2110 AATAACAGCTAGTAG 2169  
720 AA 661  
2170 AATATAGAAATGTTTCTATCAAACTTTTCATTTTAAAGAGTGAAGAGAGAGAGAG 2229  
660 AA 601  
2230 ATGTTGTTTATATATATCTCTAGAGCTTACGCTATACATGAGATTTTTCAGATTTT 2289  
600 AA 541  
2290 GATGATATTTATATAG 2349  
540 AA 481  
2350 TTAAGTACGAG 2409  
480 AA 421

QY 2410 CAAAAATACGTAATAAAAAACCGAAAAAGTCTCTTTTAGAATCGAAAAAGAA 2463  
Db 420 AA 367

RESULT 5  
CC222065 1716 bp DNA linear GSS 12-MAY-2003  
LOCUS CH261-11A13 RM1.1 CH261 Gallus gallus genomic clone CH261-11A13,  
DEFINITION genomic survey sequence.  
ACCESSION CC222065  
VERSION CC222065.1 GI:30546917  
KEYWORDS GSS.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 1716)  
AUTHORS Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E. and Wilson, R.  
Gallus gallus BAC End Reads  
Unpublished (2003)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 182000 Std Error: 0.00  
Seq primer: RM1 TAGACTCTACTATAGGGAGA  
Class: BAC ends  
High quality sequence start: 905  
High quality sequence stop: 985.

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/organism="Gallus gallus"  
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/db\_xref="taxon:9031"  
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/clone\_lib="CH261"  
/note="Vector: pTABAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
CH261 Female Chicken library - for library and clone  
ordering information: http://www.chori.org/bacpac"

ORIGIN  
Query Match 9.0%; Score 223.2; DB 28; Length 1716;  
Best Local Similarity 49.3%; Pred. No. 2.2e-18;  
Matches 637; Conservative 0; Mismatches 650; Indels 5; Gaps 2;

QY 1152 AAAGATGCAACTGGTAAAAATGCGAGACAAATATATAAGGGAAGTTCAAGGATTTTA 1211  
Db 172 AA 231

QY 1212 GAAAGATTTTAGATCCAGTAAGGTAAGTAATGCTTCAATGTCCTCAGCATGAA 1271  
Db 232 AA 291

QY 1272 TTGCGAAAAAATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331  
Db 292 AA 351

QY 1332 GCTGCTTTTTAG 1391  
Db 352 AA 411

QY 1392 TTAG 1451  
Db 412 AA 471

QY 1452 GAAGTTAAAAAG 1510









Db 1309 AAAAAAAAAAGAAAAAACAACAAAAAAGAAAAAAGAAAAAACAACAA 1368  
 Qy 2277 GATTTCAGATTTTGATGATTAATTTATATAGAAAAACAAAAAAGAAATAGATAAATCTTAT 2336  
 Db 1369 ACACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1428  
 Qy 2337 AACCAAGCTCTATTTAACTAGCCNATTAATCTTAAAGCAAAAAAGCAAAATNTTACAGTGC 2396  
 Db 1429 AAAAAACCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1488  
 Qy 2397 TGTGTAAGAGATGCAAAATACGTAATAAATAACCGGAAAAA 2437  
 Db 1489 AACCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1529

RESULT 9  
 CG756607/c  
 LOCUS  
 DEFINITION P051-4-C04.yb Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
 genomic survey sequence.

ACCESSION CG756607  
 VERSION CG756607.1 GI:37984341  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neadiplogasteridae; Pristionchus.

TITLE  
 JOURNAL Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
 Buntjer,J., van der Meulen,M. and Sommer,R.J.  
 MEDLINE An integrated physical and genetic map of the nematode Pristionchus  
 pacificus  
 PUBMED Mol. Genet. Genomics 269 (5), 715-722 (2003)  
 COMMENT 22835951

CONTACT: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel.: 00497071601371  
 Fax: 00497071601498  
 Email: raif.sommer@uebingen.mpg.de  
 Class: BAC ends.  
 Location/Qualifiers  
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 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Ppa EcoRI BAC Library"  
 /notes="The library was generated by a partial digest of  
 the genomic DNA with EcoRI and cloning into the BAC  
 vector."

FEATURES  
 source  
 1..1298  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Ppa EcoRI BAC Library"  
 /notes="The library was generated by a partial digest of  
 the genomic DNA with EcoRI and cloning into the BAC  
 vector."

ORIGIN  
 Query Match 8.5%; Score 212.2; DB 29; Length 1298;  
 Best Local Similarity 46.6%; Pred. No. 5.4e-17;  
 Matches 538; Conservative 0; Mismatches 616; Indels 0; Gaps 0;

Qy 1277 AAAAAAATTCAGAAAGAAAGAGTAAATATACGGGAGAGAGAAATGATAAGCTGT 1336  
 Db 1291 AAAAAAANNN 1232  
 Qy 1337 CTTTATTAGGAGAAAGAAATCAAAGAGGATGAAGAGAAATGAGCAAGCTGTTAATTAGA 1396  
 Db 1231 AAAAAAANNN 1172  
 Qy 1397 AGAAAAAATCCGAGAGAGATGAAGAGTTGTTAATTAGAGAGAAAGATTAAGT 1456  
 Db 1171 AAAAAAANNN 1112  
 Qy 1457 TAAAAAGAGACTCAAGAGATGAAGATAAAGAGAAATAGAGAAACAAACAAAGAACT 1516

Db 1111 NAAAAAANNN 1052  
 Qy 1517 GAAAAAGCACAAGAAAGAAAAACACACGACGACGAAAAAGAAAAAGAAAAACGAAAAACA 1576  
 Db 1051 AAAAAAANNN 992  
 Qy 1577 GCAAGAGAAAGAAACGAAAAACGACGACGACGAAAAAGAAAAAGAGAGAGCTTAAAAACAA 1636  
 Db 991 AAAAAAANNN 932  
 Qy 1637 AATTAATAAACTTCGGGATTAATAGATGAGATAGTTGGATATTTGATGCTATAGAAAG 1696  
 Db 931 AAAAAAANNN 872  
 Qy 1697 TCAAAACNAGTGTAAACCCGAAAGCAGTTATAGATAAAATTTACGGGCTGTATATGATTA 1756  
 Db 871 AAAAAAANNN 812  
 Qy 1757 TTTTACCCGATGACACCAAAAAAGCTATATATAAACATGGGGAGATTTAGAGATGAAGA 1816  
 Db 811 AAAAAAANNN 752  
 Qy 1937 AAATGTAGATGTCAGCGAAATTTAAAGAGATTTAGAAAAAGTAAATCAGGATTTAGAAAA 1996  
 Db 631 AAAAAAANNN 572  
 Qy 1997 GGTAAAGAAATATCTTAAAGCAATTTCTAAATTTGAAGAAATTAAGGATCATCAGTTA 2056  
 Db 571 AAAAAAANNN 512  
 Qy 2057 CAGTCAGTAATATATATGATGTCCTTTAGATGTAATTTTACGTCACACAAATTAAC 2116  
 Db 511 AAAAAAANNN 452  
 Qy 2117 AGCTAGTAGAAAAAGTTCACTGGCTGTATTATTTTGTAGATTTTCATTTGTTATGATAAG 2176  
 Db 451 AAAAAAANNN 392  
 Qy 2177 AATGTTTCTATCAAAACTTTTCATTTAAAGTGCACAAACTATTTGCTAAAATGTTGT 2236  
 Db 391 AAAAAAANNN 332  
 Qy 2237 TTATTTATATCTCTCTAGAGCTATGAGCTATACAAATGAGATTTTCAGATTTTGTATGATA 2296  
 Db 331 AAAAAAANNN 272  
 Qy 2297 ATTTATATAGAAACAAAAAAGAAATAGATAAACTTATAACAAGCTCTATTATACTA 2356  
 Db 271 AAAAAAANNN 212  
 Qy 2357 GCCNAATTAATCTTAAAGCAAAAAAGACAAATNTTACAGTGTGTTGAAAGAAATGCAAAAT 2416  
 Db 211 AAAAAAANNN 152  
 Qy 2417 ACGTAATAAAACC 2430  
 Db 151 AAAAAAANNN 138

RESULT 10  
 CG744327/c  
 LOCUS  
 DEFINITION P036-4-E08.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
 genomic survey sequence.  
 ACCESSION CG744327









QY	1512	GAAGTGGAAAAAGCACAAGAAAGAAAAACAACGACGAAGAAAAAGAAACAGAAAAAAACAA	1571
Db	366	AA	425
QY	1572	GAAACAGCAAGAAAGAAAAAGAAACGAAACGACACAGAACACAAAGAAAGAAAGCGAGACTAAA	1631
Db	426	AA	485
QY	1632	AACAAAATTTAAAAAACCCTTGGCGATATAAATAGATGAGATAAGTTGGAATAATTGATGGTATA	1691
Db	486	AA	545
QY	1692	GAAGAGTCAAAACAAGTGTAAAAACCGAAAGCAGTTTACGATATAAAATTACGGGGCCTGTATAT	1751
Db	546	CARAAACCCCCCCNNAAAN	605
QY	1752	GATTATTTTACCGATGACACAAAAAAAGCTATATATAAAC-----ATGGGGAGATT	1803
Db	606	CANNANAA	665
QY	1804	TAGAAGATGAAGAGCGCAAGGATTGGGAAAAATTATTGAAAGATTTCAGTGATACTAGAG	1863
Db	666	AA	725
QY	1864	ATGAGTTAAGAACCAATTTAAATTAAGATATAAAAAAAAAATATTATGCCCATGAAAAATGAGC	1923
Db	726	AA	785
QY	1924	CTCCTCTAAAGAAAAATGTAGTGTACGCGAAATTTAAAGAGAGATTTTAGAAAAAGTAAAT	1983
Db	786	AA	845
QY	1984	CAGGATTAGAAAAGGTTTAAAGAAATCTTTAAAGCAATTCCTAAATTTGAAGAAATTAAG	2043
Db	846	AA	905
QY	2044	GATACATCAGTTTACAGTCAGTAAATTAATTATTTGGATGCTTTTAGATGTAACCTABATTTTACG	2103
Db	906	AA	965
QY	2104	TACACAAAATAACAGCTAGTAGAAGAGTTCACTGGCTGTTATTTTGTGTAGATTTTCAAT	2163
Db	966	NAAAAAAAAAAAAAAAAANCAAA	1025
QY	2164	GTTATGAATATAGAAATGTTTCTCTACAAACITTCATTTTAAAGGTGCGAABACTATTG	2223
Db	1026	AA	1085
QY	2224	CTAAAAATGTGTTTATTATATCTCTCTAGAGCTATGACGTATACAAATGAGATTTCA	2283
Db	1086	NAA	1145
QY	2284	GATTTTTCATGATATTTTATTAAGAAACCAAAAAAAAAAGAAATAGTAACTTTATAACACAG	2343
Db	1146	AAAAAAAAAAAAAAAAAAAAACAAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAANA	1205
QY	2344	CTCTATTTAACTAGCCNAAATACTCTTAAAGCAAAAAAGACAAATNTACAGTGTCTGTGAA	2403
Db	1206	AA	1265
QY	2404	AGATCGAABAAATACGTAAATAAARCCGGAAGAGTGTTCTTTTAGATCGGAAAAAGAA	2463
Db	1266	AA	1325
QY	2464	TTTGTGTTAAAGACACTTTTGAAAPAGA	2487
Db	1326	AAAAAAAAAAAAAAAAAAAAACAAAAAA	1349

RESULT 14					
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LOCUS	CG747324	1211 bp	DNA	linear	GSS 24-OCT-2003
DEFINITION	P040-4-D10.2a	Ppa	EcoRI	BAC Library	<i>Pristionchus pacificus</i> genomic,

genomic survey sequence.	
ACCESSION	CG747324
VERSION	CG747324.1 GI:37968250
KEYWORDS	GSS.
SOURCE	Pristionchus pacificus
ORGANISM	Pristionchus pacificus
	Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
REFERENCE	1 (bases 1 to 1211)
AUTHORS	Srinivasan,J., Sin,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE	An integrated physical and genetic map of the nematode Pristionchus pacificus
JOURNAL	Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE	22835951
PUBMED	12884007
COMMENT	Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@uebingen.mpg.de Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..1211
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	/notes="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
ORIGIN	
Query Match	8.4%; Score 209.6; DB 29; Length 1211;
Best Local Similarity	48.4%; Pred. No. 1.2e-16;
Matches 466; Conservative	0; Mismatches 496; Indels 1; Gaps 1;
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Db	1196 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 1137
QY	1227 CCAGTAAAGGATAAAAATTGCTTCAAATGGTCCATAGCAGATGAATTCGCAAAAAAATTA 1286
Db	1136 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 1077
QY	1287 CAGAGAGAGAAAGGTAATAATACGGGGAGAGAGAAAATGATAAGCTGCTCTTTTAGGA 1346
Db	1076 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 1017
QY	1347 GAAGATTCAAAAGAGGATGAAGAAGAAAATGACAGCTGTTAATTTAGAAGAAAAAAT 1406
Db	1016 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 958
QY	1407 GCGAGAGAGATTAAGAAAGTTGTTAATTTAGAGAGAAAGAATTAGAAGTTAAAAAGAG 1466
Db	957 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 898
QY	1467 ACTGAAGAGATCAAGTAAAGAGAAATAGAGAAACAAAAACAGAGCTGGAAGAAGCA 1526
Db	897 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 838
QY	1527 CAAGAAGAAAAACAACGACAGAGAAAAAGAAACGAAAAAACAAGAAACGCAAGAGAA 1586
Db	837 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 778
QY	1587 AAGAAACGAAACGACAAAGACAAAGAAAGAGAGAGAGCTTAAAAAACAATAATTAANA 1646
Db	777 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 718
QY	1647 CTTGCGGATAAATAGATGAGATAAGCTTGGAAATTTATGATCGTTATAGAAAGTCAACAAGT 1706



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Db 717 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 658
QY 1707 GTAAACCGAAGCAGTTATAGATATAAATTTACGGGCTGTATATATATTTTACCGAT 1766
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QY 1767 GACACAAAAAGCTATATATAAAGCTGGGAGATTTAGACATGAAGAGCGGAGGA 1826
Db 597 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 538
QY 1827 TTGGGAAATTTATTGAAGAAATTCAGTGATCTAGACATGAGTTAAGAACCAAAATTTAAAT 1886
Db 537 ANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 478
QY 1887 AAGATATATAAATAATTTATGCGCATGAAATGAGCCCTCTTAAAGAAATGTAGAT 1946
Db 477 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 418
QY 1947 GTCAGCGAATTAAGAGAGATTTAGAAAAGTAAATCAGGATTAGAAAAGGTTAAAGAA 2006
Db 417 NAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 358
QY 2007 TATCTTAAAGACATTTCTAAATTTGAAGAAATTTAAAGGATACATCAGTTACAGTAA 2066
Db 357 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 298
QY 2067 TTATATTGGATGCTTTTAGATGTAACCTAAATTTTACGTACACAAATACAGCTAGTACA 2126
Db 297 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 238
QY 2127 AAA 2129
Db 237 NAA 235

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RESULT 15
CG749971/c
LOCUS
DEFINITION P044-2-E09.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION CG749971
VERSION CG749971.1 GI:37970948
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1377)
Srinivasan,J., Sins,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
12884007

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COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1. 1377
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
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/db_xref="taxon:54126"
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/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC

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Query Match 8.4%; Score 209.4; DB 29; Length 1377;
Best Local Similarity 45.6%; Pred. No. 1.2e-16;
Matches 553; Conservative 0; Mismatches 657; Indels 3; Gaps 1;

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Db 1255 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1196
QY 1167 AAAAAATCGAGAACAAATATATAAAGGGAAGTTCAAGGATTTTTCAGAAAGATTTTATAGAT 1226
Db 1195 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1136
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Db 1135 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1076
QY 1287 CAAGAAGAGAAAGTAAATTAACGGGGAAGAGAAATGATTAAGCTGTCTTTTAGGA 1346
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QY 1347 GAAGATCAAAAGAGGATGAAGAAGAAATGAGCAAGCTGTTAATTTAGAGAAATAAAT 1406
Db 1015 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 956
QY 1407 CGGAGAGAGGTAAGAAAGTTGTTAAATTTAGAGAGAGAAAGAAATTTAGAAAGTAAAGAG 1466
Db 955 ANANANANANANANANANANANANANANANANANANANANANANANANANANANANANAN 896
QY 1467 ACTGAAGAGATGAAGATAAGAAAGAAATGAGAAACAAACAAAGAGTGGGAAAGCA 1526
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Db 658 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 599
QY 1767 GACAAACAAAAGCTATATATAAACAATGGGAGATTTAGAGATGAGAGGCGGAGGA 1826
Db 598 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 539
QY 1827 TTGGGAAATTTATTGAAAGAAATTCAGTGATGATGATGATGATGATGATGATGATGAT 1886
Db 538 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 479
QY 1887 AAGATAATAAATAATTTATGCGCATGAAATGAGGCTCTCTTAAAGAAATGTAGAT 1946
Db 478 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 419
QY 1947 GTCAGCGAATTTAAAGAGAGATTTAGAAAAAGTAAATTCAGGATTAGAAAAAGTTAAAGAA 2006
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QY 2067 TTATATTGGATGCTTTTAGATGTAACCTAAATTTTACGTACACAAATTAACAGCTAGTACA 2126

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Db 298 CCTCTCCTCTTAAACAATACCATTTAACCCNTATNCCACCCTANTNTTTTCTACTCCT 239  
Qy 2127 AAAGTTCACTGGCTGTTATTTTTTTGTAGATTTCATTTGATGAAATAGAAAATGTTTC 2186  
Db 238 CAATCAAAAANTNAATCATCNACCATTCNNNTNCTNCACAATCCTTATNATACCNCNTA 179  
Qy 2187 TATCAAAACTTTTCATTTAAAAAGTGCAAAACTATTGCTAAAAATGTTGTTTATTTATAT 2246  
Db 178 NCACAAAACNTNCANNTNNAACTCAAAATATTTTCATAATATTTTCTTCTAACNCTAN 119  
Qy 2247 ACTCTCTAGAGCTATGACGTATACAAATGAGATTTTCAGATTTTTCAGATAAATTTATATAA 2306  
Db 118 TANANTNTTCACCAACCCCAAAAATAATAATATANCNCCTTAATAATAAATAAATAAAN 59  
Qy 2307 GAAAAACAAAAA 2319  
Db 58 TANCNCTTAATA 46

Search completed: July 29, 2004, 20:55:42  
Job time : 6250 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 16:08:39 ; Search time 179 Seconds  
(without alignments)  
7710.407 Million cell updates/sec

Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTTACACGAAACCTT.....TTAAGACACTTTGAAGA 2487

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197.4	7.9	1498	1	US-08-118-469A-1
2	197.4	7.9	1498	1	US-08-309-119-1
3	144.4	5.8	7218	1	US-08-232-463-14
4	136	5.5	3095	6	5231168-1
5	127.4	5.1	4766	5	PCT-US93-07261-10
6	121.8	4.9	5361	3	US-08-973-462-2
7	121.8	4.9	6152	3	US-08-973-462-1
8	117.2	4.7	774	3	US-09-461-697-187
9	117.2	4.7	819	3	US-09-461-697-185
10	117.2	4.7	1669	3	US-09-461-697-184
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12	116.6	4.7	699	3	US-09-461-697-191
13	116.6	4.7	717	3	US-09-461-697-189
14	110.2	4.4	1956	4	US-08-559-896B-1
15	110.2	4.4	1956	4	US-09-351-794A-1
16	107.8	4.3	5433	3	US-08-929-329-1
17	106.6	4.3	396	4	US-09-640-173-53
18	106.6	4.3	396	4	US-09-713-550-53
19	103.2	4.1	2223	1	US-08-257-073-4
20	102.6	4.1	19124	2	US-08-487-826B-13
21	100.6	4.0	1664976	4	US-08-916-421B-1
22	100	4.0	6866	4	US-10-204-708-20
23	98.8	4.0	3337	1	US-08-072-610-1
24	98.8	4.0	3337	2	US-08-719-822B-1
25	98.8	4.0	3337	3	US-09-092-458-1
26	96.6	3.9	240	1	US-08-628-417-6
27	95.4	3.8	2447	2	US-09-014-969-14

c	28	94.8	3.8	6306	4	US-10-204-708-50
	29	92.6	3.7	3279	3	US-08-446-137B-1
	30	90.8	3.7	1320	1	US-08-257-073-15
	31	88.8	3.6	306	3	US-09-461-697-203
c	32	88	3.5	929	4	US-09-671-317-14
	33	88	3.5	1696	4	US-09-835-811-1
c	34	87.6	3.5	1001	4	US-09-671-317-439
	35	87	3.5	1298	3	US-08-948-705-3
	36	87	3.5	1298	4	US-09-510-543-3
c	37	86.2	3.5	10467	4	US-10-204-708-2
	38	86	3.5	2394	4	US-09-800-729-33
	39	85.4	3.4	1236	2	US-08-741-134-5
c	40	85	3.4	1664976	4	US-08-916-421B-1
c	41	84.8	3.4	5562	4	US-10-204-708-63
	42	84.6	3.4	1276	3	US-09-177-325-2
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	44	84.6	3.4	1276	4	US-09-590-113-2
	45	84	3.4	1891	3	US-08-973-462-3

## ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/08118469A  
; Patent No. 5656451  
; GENERAL INFORMATION:  
; APPLICANT: Flavell, Richard A.  
; APPLICANT: Fikrig, Erol  
; APPLICANT: Lam, Tuan T.  
; APPLICANT: Kantor, Fred S.  
; APPLICANT: Barthold, Stephen W.  
; TITLE OF INVENTION: NOVEL B. BURGDOFFER POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118.469A  
; FILING DATE: 08-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/099,757  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: YU-102CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1498 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..644

Sequence 50, Appl  
Sequence 1, Appl  
Sequence 15, Appl  
Sequence 203, App  
Sequence 14, Appl  
Sequence 1, Appl  
Sequence 5, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 5, Appl  
Sequence 1, Appl  
Sequence 63, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 3, Appl





Qy 1505 AAAACAAGAGTGGAAAAAGCAAGAAAGAAACCAACGACAGAGAGAAAGAAAGCAAA 1564  
Db 1209 RRR 1150  
Qy 1565 AAAACAAGACAGCAAGAGAAAGAAAGAAAGCAAGAGAGAAAGAAAGAAAGAGG 1624  
Db 1149 RRR 1090  
Qy 1625 AGCTAAAAACAATAAAAAA 1646  
Db 1089 RRR 1068

## RESULT 4

5231168-1  
; Patent No. 5231168  
; APPLICANT: DZIEGIEL, MORTEN BORRE, MARTIN JEPSEN, SOREN;  
; VUUST, JENS, EILENECK, KLAUS, WIND, ANNETTE, JAKOBSEN, PALLE H.  
; TITLE OF INVENTION: MALARIA ANTIGEN  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/409,658  
; FILING DATE: 18-SEP-1989  
; SEQ ID NO: 1:  
; LENGTH: 3095  
5231168-1

Query Match 5.5%; Score 136; DB 6; Length 3095;  
Best Local Similarity 46.5%; Pred. No. 3.5e-15;  
Matches 631; Conservative 0; Mismatches 697; Indels 28; Gaps 5;  
Qy 1141 ATGCACTGTAAAGTGCACCTGGTAAATAATCCAGAACCAATATATAAAGGGAAGTTC 1200  
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Qy 1201 AAGGATTTTGAAGAGATTTAGATCCAGTAAAGGATAAATTCCTTCAATGGTCCAA 1260  
Db 1172 CAGAAGATGATAAATAAGAAAGTTGAACATGAATAGTAGAAGTTGAAGAAATCTAC 1231  
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Qy 1381 AAGCTGTAAATTTAGAGAAATAATTCGGAGAGAGGATGAAGAAATTTGAATTTAGAG 1440  
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Qy 1661 AGATGAGATAGTTGAATA-TTGGTGGTATAGAAAGTCAACAGAGTGAACAGAGAG 1719  
Db 1652 AAAAAGGTCAACATGAATAGTAGAGTTGAAGAAATTCCTACCAGAGATAAAAA 1711  
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Db 1712 AAGTTCACATGAATAGTAGAGTTGAAGAAATTTCTACCAGAGATATAAAATGAAAAAG 1771  
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Db 1772 TTCAACATGAATAGTAGAGTTGAAGAAATTTCTCCAGAAATTTGAAATTTGAAGAAG 1831  
Qy 1837 TATTGAAGAAATTCAGTGATCTACTAGAGATGAGTTAAGAACCAATTAATAAAGATAATA 1896  
Db 1832 TACCATCAACAAACAATAACAATGAAATATTTGAACCTATAAAACCCAGAGAAAAAGA 1891  
Qy 1897 AAAAATATTATGCCCATGAAATGAGCCTCTCTAAAGAAATGTAGATGTGACGGAAA 1956  
Db 1892 ATGAATTTAGTTTGAAGAAAGAAAGCAATTCACAGAAACCCGGTGGTACCTACATTAATG 1951  
Qy 1957 TTAAGAGAGATTTAGAAAAAGTAAAAATCAGGATTTAGAAAAAGTTTAAAGAAATCTTTAAAG 2016  
Db 1952 AAAATGAAACGTTTACTCCCAACCAATCTGAAGTGAATCCACTAAACCCAGATATAGTTC 2011  
Qy 2017 ACAATTTCTAAATTTGAAGAAATTAAGGATACATCAGTTACAGTCAGTAATTTATTTGA 2076  
Db 2012 AAATTAATAATAGTACAGAAATAAACCATAAAGAGAAACCCAGTAGTAGATGTC 2071  
Qy 2077 TGCCTTTTAGATGTAACTAAAAATTTTACGTACACAAAAATAACAGCTAGTAGAAAAAGTTCACT 2136  
Db 2072 CAAAACATGTAGACAAATAATATACAGAGATGATA---ATGATGAAGAGGATGATGAT 2127  
Qy 2137 GCGTGTATTTTGTGAGATTTCAITGTTATGAATATAGAAATGTTTCTCTCAAAACT 2196  
Db 2128 GATATAGATTTTGAAGGATTTATCAAGAAAAAGATGATGAAAAAGGATTCATCAAAATAAAAT 2187  
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Qy 2257 GCTATACGTATACAAATGAGATTTGAGATTTTGTATGATGATATTTATATAAGAAAAA 2316  
Db 2248 ACTATTGTAAGTGTATGATTAATGATATGATGATGATGATGATGATGATGATGATGAT 2307  
Qy 2317 AAGAAATAGATAAATCTTATAACAGCTCTTATTAAGTACCCAACTCTCTAAAGCAA 2376  
Db 2308 AAGAAATAGCAAGATATAGTAATTTTCCAAAAATTTAAATTAATTAACAAAAA 2367  
Qy 2377 AAAAGACAAATNTACAGTCTGCTGTTGAAGAAATGCAAAATACGTAAATAAAGCCGAAA 2436  
Db 2368 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2427  
Qy 2437 AGTCTTTTGTAGATCGGAAAAAGATTTGTTAAA 2472  
Db 2428 AATATTATTTAATAAATAATATATATATATATAA 2463

## RESULT 5

PCT-US93-07261-10  
; Sequence 10, Application PC/TUS9307261  
; GENERAL INFORMATION:  
; TITLE OF INVENTION: PEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John H. C. Blasdale  
; STREET: One Giralda Farms  
; CITY: Madison  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07940-1000  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07261  
; FILING DATE: 19930805



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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/927,531
/ FILING DATE: 07-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Blasdale, John H. C.
/ REGISTRATION NUMBER: 31,895
/ REFERENCE/DOCKET NUMBER: DX0288K
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-822-7398
/ TELEFAX: 201-822-7039
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4766 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna to mRNA
/ ORIGINAL SOURCE:
/ ORGANISM: Plasmodium falciparum
/ STRAIN: Malayan Camp
/ IMMEDIATE SOURCE:
/ CLONE: p2b1/p12-1
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3..4766
/ CDS-UT593-07261-10
/

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Best Local Similarity	48.6%	Pred.	No. 1.2e-13;						
Matches	440;	Conservative	0;	Mismatches	456;	Indels	9;	Gaps	3;
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Db	3000	AAAGAAATGCAGAGCTTAAAAATAAAGAAATTACGAAATAAAGATCTGAAGATTAAAA	3059						
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Db	3177	AAATGCAGAACTAAAAAATAAGAAATTAACAAAATAAAGGATCTGAAGATTTAAAGAAAAT	3233
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Db	3237	GCAGAATTAAAAAATAAAGAAATTACAAAATAAAGGATCTGAAGGATTTAAAGAAAAATGCA	3296
QY	1875	ACCAAAATTAATAAAGA---TAATAAAAAATATTATGCCCATGAAAATGAGCTCCTCTTA	1931
Db	3297	GAGCAAAAAAATAAAGAAATTACAAAATAAAGGATCTGAAGGATTTAAAGAAAAATGCAGAA	3356
QY	1932	AAAGAAAAATGTAGATCTCAGCGAAATTTAAAGAAAGATTTAGAAAAAGTAAAAATCAGGATTA	1991
Db	3357	TTAAAAAATAAAGAAATTCGAAATAAAGGATCTGATGGATTTAAAGAAAAATGCAGAGCTA	3416
QY	1992	GAAGAGGTTAAAGAAATATCTTAAAGCAATTCCTAATTTGAAGAAATTTAAAGATACATC	2051
Db	3417	AAAATAAAGAAATTACGAAATAAAGGATCTGATGGATTTAAAGAAAAATGCAGAAATTA	3476
QY	2052	AGTTA 2056	
Db	3477	AATAA 3481	

RESULT 6

US-08-973-462-2

; Sequence 2, Application US/08973462B

; Patent No. 6191270

; GENERAL INFORMATION:

; APPLICANT: DRUILHE, PIERRE

; APPLICANT: DAUBERSIES, PIERRE

; TITLE OF INVENTION: MAJALIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

; FILE REFERENCE: 0660-0125-0 PCT

; CURRENT APPLICATION NUMBER: US/08/973,462B

; CURRENT FILING DATE: 1998-02-06

; EARLIER APPLICATION NUMBER: PCT/FR96/00894

; EARLIER FILING DATE: 1996-06-12

; EARLIER APPLICATION NUMBER: FR 95/07007

; EARLIER FILING DATE: 1995-06-13

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 5361

; TYPE: DNA

; ORGANISM: P. falciparum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(5361)

US-08-973-462-2

Query Match	4.9%;	Score 121.8;	DB 3;	Length 5361;
Best local Similarity	45.6%;	Pred. No. 1.1e-12;		
Matches 592;	Conservative 0;	Mismatches 689;	Indels 18;	Gaps 4;
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Db	4053	TGAAACAGATATTTTAGAGAGAGAAAAGAAATAGAAAAGATCATTTTGAAAAAATTCGA	4112	
QY	1202	AGCATTTTTAGAAAAGATTTTATGATCCAGTAAAGGATAAAAATTGCTTTCAAAATGGTGCCAAAT	1261	
Db	4113	AGAAGAGCTGTAAGAAATAAAAAGATCTTGAAGCAGATATATTAAAGAAGATGATCTTTCAAT	4172	
QY	1262	AGCAGATGAATTCGCAAAAAAATTTACAAGAAGAAGAAAAGGTAAATATACGGGGAAGAAGA	1321	
Db	4173	AGAAGTTGAAGAAGAAAAAATTTAGAAGAAGTACACGAATTTAAAGAAGAGGTGAACA	4232	
QY	1322	AAATGATAAAGCTGCTTTTTTAGGAGAGAATCAAAAGAGGATGAAGAGAAATGAGCA	1381	
Db	4233	TATAATAGTGGTGTATGCCCATATAAAGGTTTGGAGAAGATGATTTAGAA-----GA	4286	
QY	1382	AGCTGTTAATTTTAGAAGAAAAAATTCGGGAAGAGGATTAAGAAGTGTGTTAAATTTAGAAGA	1441	
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 1562 AAAAAACAAGACAGACAG 1621  
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 4464 AAGAGCTCAAGAGCCTTAAGTTGGAGAGAGATTTATTAAGAAGAGAGTTAAGAAGAGCC 4523  
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 1622 GAGAGCTTAAAAAACAATAAATTAACCGATGACACAAAAAGCTTATATATAAAGAGTTGGAATAT 1681  
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 4524 AAGAAAAAATAACAAAAAAGAAAGTAAGTTTGATATTAAGGATAAGGAACCAAAAGA 4583  
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 1682 TGATGTTATGAAGTCAACACAGTGTAAACCGAAGCAGTTATAGATAAATTTACGGG 1741  
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 1742 GCCTGTATATGATTTTACCGATGACACAAAAAGCTTATATATAAAGAGTTGGAATAT 1801  
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 4638 AGATATAGAGAGATATAGAGAGAGATTAAGTTGAAGATATAGATCAAGATATAGATGA 4697  
 Qy |||||  
 1802 TTTAGAGATGAAGAGCGGAGAGATTTGGGAAATTTATGAAGAGATTTGAGTGATAGTAG 1861  
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 4698 AGATATAGTCAAGACAAAGATGAAGTTATAGATTTAATAGTCCAAAAAGAGAGAGAGAT 4757  
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 1862 AGATGCTTAAGACCAAAATTAATAAAGATATAAATAATATATGCCCCATGAAATGA 1921  
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 4758 TGAAGAGTTTAAGCGGAAAGAGAGAGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4817  
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 1922 GCCTCTCTAAAAAGAAATGTAGATGTACGCGAAATTTAAAGAGAGATTTAGAAAAAGTAA 1981  
 Db |||||  
 4818 TCTTAAAAAACAAGTACGAGAGAGTAAATGAAATATGTTCAAAAAATTCATAAAGAGAGTGA 4877  
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 1982 ATCAGGATTAGAAAGTTTAAAGATATCTTAAAGCAATCTCAA---TTTGCAGAAAT 2038  
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 4878 TAAAGAGATCTTAAAGCTTTAGATCAAAAAATGATGTTACTAATGTTTAAAGCAAAA 4937  
 Qy |||||  
 2039 TAAAGGATACATCAGTTTACAGTCAGTAAATTTATTTGATGCTTTTATAGATGTAACTAAAT 2098  
 Db |||||  
 4938 TCAAGATTTTATAGTAAAGTTTAAAGCTTCGTAAGAAAAATATAAAGTATTTCTGCACC 4997  
 Qy |||||  
 2099 TTAGCTACACAAATAACAGCTAGTAGAAAGTTCTAGCTGTTATTTTGTAGATT 2158  
 Db |||||  
 4998 ATTCTATCTGCCGTTGCAGCATTTGCATCATATGTAGTTGGTCTCTTACATTTTCTTT 5057  
 Qy |||||  
 2159 TCATTGTTATGAATATAGAAATGTTTCTTATCAAACTTTCAATTAAGAGTCAAAAGTCAAA 2218  
 Db |||||  
 5058 ATTTTCATCATGTACATAGCTCTTCAACTTACTTATCAAAAGTTGACAAAC 5117  
 Qy |||||  
 2219 TATGCTTAAAGATGTTTATTTATATCTCTAGAGCTATGAGCTATACAAATGAGA 2278  
 Db |||||  
 5118 TATAAATAAATAAAGAGAGAGAGCGTTTATTTTATTTGATTTTATTTGATTTTAAAGAAATTT 5177  
 Qy |||||  
 2279 TTTTCAGATTTTGTATGATAATTTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2338  
 Db |||||  
 5178 AAAAAATTATTAACAAATGAAG 5237  
 Qy |||||  
 2339 ACAAGCTCTTTTATAGCCNATATCTCTAAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAG 2398  
 Db |||||  
 5238 AGAAGTAAACAAACAAAGCTGAG 5297  
 Qy |||||  
 2399 TTGAAGAGTGAAG 2437  
 Db |||||  
 5298 AACAACTAAGATTGATTAATAAATATAAAGTACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 5336

RESULT 7  
 US-08-973-462-1  
 ; Sequence 1, Application US/08973462B  
 ; Patent No. 6191270

GENERAL INFORMATION:  
 ; APPLICANT: DRUILHE, PIERRE  
 ; APPLICANT: DAUBERSIES, PIERRE  
 ; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES  
 ; FILE REFERENCE: 0860-0125-0 PCT  
 ; CURRENT APPLICATION NUMBER: US/08/973,462B  
 ; EARLIER FILING DATE: 1998-02-06  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/00894  
 ; EARLIER FILING DATE: 1996-06-12  
 ; EARLIER APPLICATION NUMBER: FR 95/07007  
 ; EARLIER FILING DATE: 1995-06-13  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 6152  
 ; TYPE: DNA  
 ; ORGANISM: P. falciparum  
 ; US-08-973-462-1

Query Match 4.9%; Score 121.8; DB 3; Length 6152;  
 Best Local Similarity 45.6%; Pred. No. 1.1e-12;  
 Matches 592; Conservative 0; Mismatches 689; Indels 18; Gaps 4;

Qy 1142 TGCACACTGTTAAAGATCGAACTGGTAAATAATCGAGACAAATAATATAAAGGAAAGTTCA 1201  
 Db |||||  
 4297 TGAACACAGATATTTTAGAAG 4356  
 Qy |||||  
 1202 AGGATTTTGTAGAAAGATTTTAGATCCAGTAAAGGATATAAATTTGCTTCAATGGTCCAA 1261  
 Db |||||  
 4357 AGAAGAGCTCAAGAAATATAAGATCTTGAAGCAGATATATTAAGAGAGATGATCTTCAAT 4416  
 Qy |||||  
 1262 AGCAGATGAATTCGCAAAAAATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321  
 Db |||||  
 4417 AGAAGTTGAAG 4476  
 Qy |||||  
 1322 AAATGATAAAGCTCTCTTTTGTAGAGAGAGAGATCAAAAGAGAGATGAAGAGAGAGAGAGAG 1381  
 Db |||||  
 4477 TATAATAGTGTGATCGCATATAAAGGTTTGGAGAGAGATGATTTAGAA-----GA 4530  
 Qy |||||  
 1382 AGCTGTTAATTTAG 1441  
 Db |||||  
 4531 AGTAGATGATTTAAAGAGAGAGATATATAGACATGTTAAAGGAGAGATGGAATTTAGGGGA 4590  
 Qy |||||  
 1442 GAAAGATTTAGAGTTTAAAGAGAGAGCTGGAAGAGATGAAGATGAAGATAAAGAGAGAGAGAG 1501  
 Db |||||  
 4591 TATGATAAGAGAGATTTAG 4647  
 Qy |||||  
 1502 ACAAAACAAGAGTGGAG 1561  
 Db |||||  
 4648 CTTAAAGATGTTTATCTAGTGCATTTAGGCATGGATGAAGAGAGAGAGAGAGAGAGAGAGAG 4707  
 Qy |||||  
 1562 AAAAAACAAG 1621  
 Db |||||  
 4708 AAAAGCTCAAG 4767  
 Qy |||||  
 1622 GAGAGCTTAAAAACAATAATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1681  
 Db |||||  
 4768 AAG 4827  
 Qy |||||  
 1682 TGATGTTATAGAGAGTCAACAGAGTGTAAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1741  
 Db |||||  
 4828 TGAATAGTAGAGAGTGAAG 4881  
 Qy |||||  
 1742 GCCTGTATATGATTTTATCCGATGACACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1801  
 Db |||||  
 4882 AGATATAGAGAGAGATATAG 4941  
 Qy |||||  
 1802 TTTAG 1861  
 Db |||||  
 4942 AGATATAGGTGAG 5001  
 Qy |||||  
 1862 AGATGAGTTAAG 1921

Db 5002 TGAAGGTTAAAGCGGAAAGAAAAATAGAAAAAAGTTGAAGAAAGTGTAGTGG 5061  
Qy 1922 GCCTCCTCTAAAAGAAAATCTAGATGTCAGCGAAATTAAGAGAGATTAGAAAAAGTAAA 1981  
Db 5062 TCTTAAAAACACGTAGACGAGTAAATGAATATGTTCAAAAAATGATAAAGAGTTGA 5121  
Qy 1982 ATCAGGATTAAGAAAGTTAAAGATATCTTAAGACAAATCTTAAA- --TTTGAAGAAAT 2038  
Db 5122 TAAAGAGTATCTTAAAGCTTTAGAAATCAAAAAATGATTTACTAATGTTTAAAAACAAA 5181  
Qy 2039 TAAAGGATCATCAGTACAGTCAAGTAAATATATATTGATGCTTTTATGATGTAACTAAT 2098  
Db 5182 TCAAGATTTTTTTAGTAAAGTTAAACCTTCGTAAGAAATATAAAGTATTTGCTGCACC 5241  
Qy 2099 TTACGTACACAAAATTAACAGCTAGTAGAAAGTTCACTGGCTGTATTTTTTTTGTAGATT 2158  
Db 5242 ATTCATATCTGCGTTGCACATTTGCATCATATGATGTTGGTCTCTTACATTTCTTT 5301  
Qy 2159 TCATTGTTATGATATAGAAATGTTTCTATCAAACTTTTCATTTAAAAAGTGCAAAAC 2218  
Db 5302 ATTTTCATCATGTGTAAACATAGCTTCTTCACTTACTTATTATCAAAAAGTTGACAAAAC 5361  
Qy 2219 TATTGCTTAAAAATGTTGTTTATTTATATATCTCTAGAGCTATGAGTATACAAATGACA 2278  
Db 5362 TATAAATRAAAATAGGAGAGACCGTTTATTCACTTTGATTTGATCTTTTAAGAAATTT 5421  
Qy 2279 TTTTCAGATTTGATGATAATTTATATAAGAAAACAAAAAGAAATAGATAAACTTATAA 2338  
Db 5422 AAAACATTTATTTACAAATGAAGAAAAATTTAGTAAGAAAAAATAAATATGTAAT 5481  
Qy 2339 ACAAGCTCTATTTAACTAGCCNATTAACCTTAAGCAAAAAAGACAAATNTACAGTCTG 2398  
Db 5482 AGAAGTAAACAAAGCTGAGAAAAAAGGTAATGTACAGGTAAACAAATAAAACCGAGAA 5541  
Qy 2399 TTGAAGAAATGCAAAAATACGTAAATAAAACCGGAAAAA 2437  
Db 5542 AACAACTAAAGTTGATAAAAAATATAAGTACCGAAAAA 5580

## RESULT 8

US-09-461-697-187  
; Sequence 187, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Puranam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 187  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-461-697-187

Query Match 4.7%; Score 117.2; DB 3; Length 774;  
Best Local Similarity 50.3%; Pred. No. 4.9e-12;  
Matches 324; Conservative 0; Mismatches 308; Indels 12; Gaps 1;

Qy 1035 AAAAAATGAAAAATTTATTTATTTGCTGTGTTTGTCTGATAGTTCTTGCAAGATT 1094  
Db 55 ABAATGAGACAAAAAGTATGATGGAAGAAAAACATAGATACAGTCCCAAGCAGTT 114

Qy 1095 GATCAACTGCTAAAGATGCAACTCGTAAAGATGCAACTCGTAAAGATGCAACTCGTAA 1154  
Db 115 GCTGAACCAAGCAAGCAAGTGTGTTGAAGAGACTACATGAAATGCTTAAAAATGGA 174  
Qy 1155 GATCAACTGCTAAAGATGCAAGCAAAATATAAAAGGAAAGTTCAAGGATTTTGA 1214  
Db 175 GAAGCCAAATTCACAGAGGCCACAGCTTCTGAAAAAGAAATTTGTGGAAGTAAAAAGAA 234  
Qy 1215 AAGATTTTATGATCCAGTAAAGGATAAAATTCCTTCAATGCTCCAAATAGCAG- - - - - 1266  
Db 235 AATATTGAGATGCCACGAAAGGGAGGAGAAAGAAAGAGCGTGGCAGCAGAGTA 294  
Qy 1267 - - - - -ATGAATTTGGCAAAAAAATTACAAGAGAAAGAAAGTAAATAACGGGAAAGAA 1322  
Db 295 AAAAATGAAGAAAGATCAGAAAGAGATGAAGAGAGATCAAAACGAAGAGAAAGGGAA 354  
Qy 1323 AATGATAAGCTGCTCTTTTATAGGAGAGAGATCAAAAGAGGATGAAGAGAAATGACCA 1382  
Db 355 GCTGGAAGAAAGACAAAGATGAAAGAGGGGAGAGATGGAAGAGGATAAAAATGGA 414  
Qy 1383 GCTGTTAATTTAGAGAAAAAATCGGAGAGAGATGAAGAAAGTTGTTAATTTAGAAG 1442  
Db 415 AATGAGAAAGGAGAGATGCAAAAGAGAGAGATGGAAAAAAGGTGAAGACGGA 474  
Qy 1443 AAGAAATTTAGAACTTAAAAAGAGACTGAAGAGATGAAGTAAAGAGAAATAGAGAA 1502  
Db 475 GGAATGAGAGATGGAAGAAAGAGAGAGATGAAAGAGAGAGATGAAAGAGAGAGAGAG 534  
Qy 1503 CAAAAACAAGAAAGTGGAAAAAGCACAAGAAAGAAACAAACGACAAAGAAAGAAACGA 1562  
Db 535 GAACAGAGTTGGAAGAGAGATGAAGATGGAAGAGAGAGAGAGAGATAAAAAGAGGG 594  
Qy 1563 AAAAAACAAGAACAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1622  
Db 595 AAGATGTTAAAGTCAAGAGAGATGAAAAAGAGAGAGAGATGAAAAAGAGAGATGAAG 654  
Qy 1623 AGAGCTAAAAACAAAATTTAAAAAATTCGCGATATAATAGATGA 1666  
Db 655 GGAATGAGGAAGAGCTGGAAGAGAGAGAGAGAGAGATTTAAAGA 698

## RESULT 9

US-09-461-697-185  
; Sequence 185, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Puranam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 185  
; LENGTH: 819  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-461-697-185

Query Match 4.7%; Score 117.2; DB 3; Length 819;  
Best Local Similarity 50.3%; Pred. No. 5e-12;  
Matches 324; Conservative 0; Mismatches 308; Indels 12; Gaps 1;

Qy 1035 AAAAAATGAAAAATTTATTTATTTGCTGTGTTTGTCTGATAGTTCTTGCAAGATT 1094  
Db 55 ABAATGAGACAAAAAGTATGATGGAAGAAAAACATAGATACAGTCCCAAGCAGTT 114

Db 100 A A A A T G A A G C A A A A A G T G A T G A T G G A A G A A A A C A T A G A T C A A G T C C C C A A G C A G T T 159  
 Qy 1095 G A T G C A A C T G T T A A G A G T C A A C T G T T A A G A G T C A A C T G T T A A G A G T C A A C T G T T A A 1154  
 Db 160 G C T G A A A C C A A G C A A G A A G C A G T T G T T G A A G A G C T A C A A T G A A A T G C T T A A A A T G G A 219  
 Qy 1155 G A T G C A A C T G T T A A A A T C A G A A C A A A T A T A A A A G G A A A G T T C A A G A T T T T A G A A 1214  
 Db 220 G A A G C A A A A T T A C A G A G G C A C A G T T C T G A A A A A A A A T T G T G A A G A T A A A A G A A G A A 279  
 Qy 1215 A A G A T T T A G A T C C A G T A A A A G T A A A A T T G C T T C A A T G G T C C A A T A G C A G - - - - - 1266  
 Db 280 A A T A T T A G A T G C C A G A A A A G G A A A G G A A A A G A A A G A A G A A G C A G T G C C A G A A G T A 339  
 Qy 1267 - - - - - A T G A A T T G C A A A A A A A T T A C A A G A A A A A A A G T A A A T A A C G G G A A A G A A A 1322  
 Db 340 A A A A T G A A G A A G A G A T C A G A A A G A A G A T G A G A A A G A T C A A A C C G A A G A A A G G G A A 399  
 Qy 1323 A A T G A T A A A G C T G T C T T T T T A G A G A A G A A T C A A A A G A G A T C A A A A A A A A A T G A C A A 1382  
 Db 400 C T G G A A A G A A C A A A A G A T G A A A A G G G A A A A G A T G G A A A G A G A T A A A A T G G A 459  
 Qy 1383 G C T G T T A A T T A G A A A A A A A A T G C G A A G A G A T A A G A A A G T T T T A A T T A G A A G A G 1442  
 Db 460 A A T G A A A A G A G A A G A T C A A A A G A A A A A G A A G A T G G A A A A A A A A A G T G A A G A C G A A A 519  
 Qy 1443 A A A G A T T A G A A G T T A A A A A G A G A C T G A A G A G A T G A A A A A A A A A A A A A A A T A G A A A 1502  
 Db 520 G G A A T G G A G A G A T G A A A A G A A A A A G A A G A G A T G A A A A G A G A A A G A A A A A A A A 579  
 Qy 1503 C A A A A C A A A A G T G A A A A G C A C A 1562  
 Db 580 G A A C A G A G T T G A A A A G A G A T G A A T G G A 639  
 Qy 1563 A A A A A C A A A C A G C A G A G A 1622  
 Db 640 A A A G A T G T A A A G T C A 699  
 Qy 1623 A G A G C T A A A A C A A A A T T A 1666  
 Db 700 G G A A T C A G A A G A G C T G G A A A A G A 743

RESULT 10  
 US-09-461-697-184  
 ; Sequence 184, Application US/09461697  
 ; Patent No. 6277974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Purnam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; FILE OF INVENTION: CELL DEATH  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/461,697  
 ; CURRENT FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 184  
 ; LENGTH: 1669  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-461-697-184

Query Match 4.7%; Score 117.2; DB 3; Length 1669;  
 Best Local Similarity 50.3%; Pred. No. 5.6e-12;  
 Matches 324; Conservative 0; Mismatches 308; Indels 12; Gaps 1;

Qy 1035 A A A A A A T G A A A A T T T A T T A T T T G C T G T A T T T T G C T G T A A G T T C T T C C A A G A T T 1094  
 Db 179 A A A A T G A A G C A A A A A G T G A T A T G A T G A A A A A A A C A T A G A T C A A G T C C C A A G C A G T T 238  
 Qy 1095 G A T C A A C T G T T A A A G A T C A A C T G T T A A A G A T G C A A C T G T T A A A G A T G C A A C T G T T A A 1154  
 Db 239 G C T G A A A C C A A G A A G C A G T T G T T G A A G A A G A C T A C A A T G A A A A T G C T A A A A T G G A 298  
 Qy 1155 G A T C A A C T G T T A A A A T T C A G A A C A A A A T A T A A A A G G A A A G T T C A A G A T T T T A G A A 1214  
 Db 299 G A A C C A A A A T T A C A G A G C A C C A G T T C T G A A A A A A A A A T T G T G A A G T A A A A G A A G A A 358  
 Qy 1215 A A G A T T T A G A T C C A G T A A A A G A T A A A A T T G C T T C A A A T G C T C A A T A G C A G - - - - - 1266  
 Db 359 A A T A T T C A A G T C C C A G A A A A A G G G A G A 418  
 Qy 1267 - - - - - A T G A A T T G C A A A A A A A T T A C A A A A G A A A A A G T A A A T A A C G G G A A A G A A A 1322  
 Db 419 A A A A T G A A A G A A G A T C A A A A G A A G A T G A A A A G A T C A A A A C C G A A G A A A G G G A A 478  
 Qy 1323 A A T G A T A A A G C T G T C T T T T T A G A G A A G A A T C A A A A G A G A T C A A A A A A A A A A T G A C A A 1382  
 Db 479 G C T G A A A A G A A A A A G A T G A A A A A G G G A A A A G A T G C A A A A A A A A A A A A A A A A A A 538  
 Qy 1383 G C T G T T A A T T A G A A A A A A A A T G C G A A G A G A G A T A 1442  
 Db 539 A A T G A A A A G A A G A A G T C A A A A A G A 598  
 Qy 1443 A A A A A T T A G A A G T T A 1502  
 Db 599 G G A A T G G A A A G A T G G A 658  
 Qy 1503 C A A A A C A A A A G T G A 1562  
 Db 659 G A A C A G A G T T G G A A A A G A A T G A A T G G A 718  
 Qy 1563 A A A A A C A A A C A G C A G A 1622  
 Db 719 A A A G A T G T A A A G T C A 778  
 Qy 1623 A G A G C T A A A A C A A A A T T A 1666  
 Db 779 G G A A T C A G A A G A G C T G G A A A A G A 822

RESULT 11  
 US-09-461-697-193  
 ; Sequence 193, Application US/09461697  
 ; Patent No. 6277974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Purnam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; FILE OF INVENTION: CELL DEATH  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/461,697  
 ; CURRENT FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 193  
 ; LENGTH: 696  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-461-697-193

Query Match 4.7%; Score 116.6; DB 3; Length 696;  
 Best Local Similarity 51.3%; Pred. No. 6.1e-12;



Db 66 CAAGCAAGAGCAGCTGTTGCAAGAGCAGTACAAATGAAATGCTAAATAATGAGAGCCAA 125  
Qy 1148 TGGTAAAGATGCACTGGTAAAAATCGAGAACAAATATATAAGGGAAAGTTCAAGATT 1207  
Db 126 AATTACAGAGCCACAGCT--TCTGAAAAAGAAATTTGGAAGTAAAGAGAAATAT 182  
Qy 1208 TTTAGAAAGATTTAGATCCAGTAAAGGATAAATTTGCTTCAATGGTCCCAATAGCAG 1267  
Db 183 TGAAGATGCCACAGAAAGGGAGAGAAAGAAAGAGCGAGTGGCAGCAGAGTAAAAA 242  
Qy 1268 TGAATTCGCAAAAAATTAACAAGAGAAAGAAAGGTAATTAACCGGGAGAGAGAAATGA 1327  
Db 243 TGAAGAAAGAGATCAGAAAGAGATGAAGAGATCAAAACGAAAGAGAGAAAGGGAGCTGG 302  
Qy 1328 TAAAGCTGCTTTTAGGCAAGAAATCAAAAGAGAGATGAAGAGAAATGACCAAGCTGT 1387  
Db 303 AAAGAAGACAAAGATGAAGAAAGGGAGAGAGATGGAAGATGGAAGAGAGATGAAGATGA 362  
Qy 1388 TAATTTAGAGAAAAAATCGGAGAGAGATGAAGAAAGTTGTTTAATTTTAAAGAGAAAGA 1447  
Db 363 GAAAGGAGAGATGCAAAAGAGAAAGAGATGCAAAAGAAAGGTGAAGACGGAAGAGAA 422  
Qy 1448 ATTAGAGTTAAAGAGAGCTGAAGAGATGAAGATGAAGAGAAATAGAGAAACAA 1507  
Db 423 TGGAGAGATGGAAAGAGAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482  
Qy 1508 ACAAGAGTGGAAAGACCAAGAGAGAAACCAAGCAAGAGAGAGAGAGAGAGAGAGAGAG 1567  
Db 483 AGGAGTTGGAAGAGAGATGAAGATGGAAGAGAGAGAGAGATGAAGAGAGAGAGAGAG 542  
Qy 1568 ACAAGACAG 1627  
Db 543 TGTAAAGTCAAGAGATGAAG 602  
Qy 1628 TAAAGCAAAATTAAGAACTTCGGATAAATAGATGA 1666  
Db 603 TGAGGAGAGCTGGAAAGAGAGAGAGAGAGAGATTAAGAGA 641

## RESULT 14

US-08-559-896B-1  
; Sequence 1, Application US/08559896B  
; Patent No. 6310046  
; GENERAL INFORMATION:  
; APPLICANT: Patrick E. Duffy  
; APPLICANT: Christian F. Ockenhouse  
; TITLE OF INVENTION: SEQUESTIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John Moran  
; STREET: USA NMC MCMR-JA  
; CITY: FORT DETRICK, FREDERICK  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/559,896B  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Moran, John  
; REGISTRATION NUMBER: 26,313  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1956 base pairs  
; TYPE: Nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; US-08-559-896B-1

Query Match 4.4%; Score 110.2; DB 4; Length 1956;

Best Local Similarity 45.1%; Pred. No. 9.4e-11; Indels 30; Gaps 5;  
Matches 633; Conservative 0; Mismatches 740;

Qy 1079 AAGTTCCTTGCAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1138  
Db 528 AATTATAGTATGTATAGAGATATAAGTAAACAAAATATAAAGACCTTAATTAATAA 587  
Qy 1139 AGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1198  
Db 588 TGAAGAGAAACAAATTAAGGATATAAAGGATATAAAGGATATAAAGGATATAAAGGAT 647  
Qy 1199 TCAAGGATTTTGAAGAGATTTTAGATCCAGTAAAGGATATAAAGTTCCTTCAATGGTCC 1258  
Db 648 AAAAAAGATATAGATATAGATGTAGACATAGATATAAGATATACATAAAGATCATGTAGA 707  
Qy 1259 AATAGCAGATGAATTCGCAAAAAATTTACAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1318  
Db 708 AGAATTTATACGAGAGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGGAT 767  
Qy 1319 AGAATGATTAAGCTGCTCTTTTAGGAGAGAGATCAAAAGAGAGATCAAAAGAGAGATCA 1378  
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Qy 1379 GCAAGCTGTTAATTTAGAAG 1438  
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Qy 1439 AGAGAGAGATTTAGAGATTTAAAGAGAGATTTAGAGAGAGATTTAGAGAGAGAGAGAGAG 1498  
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Qy 1499 GAAACAAAAACAAGAGTGGAG 1558  
Db 948 TAAATATATGAGAGAGATTTAAACAAATGAGTATGATGAATTTCAACATGTAGAGAG 1607  
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Qy 1619 AAGGAGAGCTAAAAACAAGATTTAAAGATTTGCGGATATAAAGATTTAGATGAGATAGT 1678  
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Qy 1799 AGATTTAGAGATGAAG 1858  
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Db 1290 AATTAATAG 1349  
Qy 1919 TGAGCTCTCTTAAAG 1978  
Db 1350 AATTTAG 1409

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Db 1410 AATTAAAAAGACAAAAAGTTAATGTTCCATATAGTGAATTTTAAATTCAAAAGT 1469
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QY 2089 TAACTAAATTTTACGTACACAAATTAACAGCTAGTAGAAAAGTTCACTGGCTGTTATTTT 2148
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QY 2209 GTCCAAAACTATGCTTAAATGTTGTTTATTTATATCTCTCTAGAGCTATGAGTAT 2268
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QY 2269 ACAATCAGATTTTCAGATTTTGTATGATATTTATATACTCTCTAGAGCTATGAGTAT 2328
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Db 1888 GCGGAGAAAAAACCAAACTTTGA 1910

RESULT 15
US-09-351-794A-1
; Sequence 1, Application US/09351794A
; Patent No. 6641815
; GENERAL INFORMATION:
; APPLICANT: DUFFY, PATRICK E.
; APPLICANT: OCKENHOUSE, CHRISTIAN P.
; TITLE OF INVENTION: SEQUESTRIN
; FILE REFERENCE: 38644-175519
; CURRENT APPLICATION NUMBER: US/09/351,794A
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 08/559,896
; PRIOR FILING DATE: 1995-11-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 1
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-351-794A-1

Query Match 4.4%; Score 110.2; DB 4; Length 1956;
Best Local Similarity 45.1%; Pred. No. 9.4e-11;
Matches 633; Conservative 0; Mismatches 740; Indels 30; Gaps 5;

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QY 1199 TCAAGGATTTTACAAAGATTTTATAGTCCAGTAAAGGATATAAAGTCTTCAATGCTCC 1258
Db 648 AAAAAAGATATAGATATAGATGTAGACATAGATATAAAGATCATGTAGA 707
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Db 768 AGACGCATTTATATAGAGTATACCTTAGAAGAAATTAGATAGATGAACAGAGACGAATTATA 827
QY 1379 CCAAGCTGTTAAATTTAGAAAGAAAAAATGCGGAAGAGGATAAAGAAAGTTGTTAAATTAGA 1438
Db 828 TAGAGTATACCTAGAGAAATTTAGAAAAAATAGACAAGAGAAAAAGAAAAATTCATAG 887
QY 1439 AGAGAAAGAAATTAGAGCTTAAAAAAGAGACATGAAGAAGATGAAGATAAAGAGAAAAATGA 1498
Db 888 AGAAAAATTTACAAAAATTTGAAAAAGAGAAAAATTAATAAAAAATGATTAAGATCAAAATAGA 947
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QY 1859 TAGAGATGAGTTAAGAACCAAAATTAATAAAGATAATAAAAAATATTTATGCCCATGAAAA 1918
Db 1290 AATATAAAGCACACAAATAATAATTAATGAAAAATGTAGAAATTTAGATTTAGTTGACG 1349
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Db 1350 AATTTAGACAAGGATAAAGGAGCCCAAGATAGAGATATATAGACTATTTTAAACAAAGA 1409
QY 1979 AAAATCAGGATTAGAAAAAGGTTAAAGAAATATCTTAAAGACAATTCCT-----AAAT 2028
Db 1410 AATTAAAAAGACAAAAATGTTAATGTTTCCAATATAGTGAATTTTAAATTCAAAAAGT 1469
QY 2029 TTGAAGAAATTAAGGATACATCAGTTTACAGTCAGTAAATATATTTGGATGCTTTTAGATG 2088
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QY 2209 GTGCAAAACTATTCCTAAAAATGTTGTTTATTTATATCTCTCTAGAGCTATGAGTAT 2268
Db 1648 AAAAATGTTGGAGATATAAAGAGTGTGGAGATATAAAGAGTGTGATGATATAAACAAT 1707
QY 2269 ACAATAGAGATTTTCAGATTTTATGATATAATTTATATAAAGAAACAAAAAGAAATAGAT 2328
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Qy	2329	AACTTATAACAAGCTCTATTAACTAGCCNAACTAACTCTAAAGCAAAAAAGACAAATN	2388
Db	1768	GGTATAACAATGTGGGAGATATAAACAATGTGGGAGATACAAATAATGCTGGAGATATA	1827
Qy	2389	TACAGTGTCTGTGAAGAATGCRAAAATACGTAATAAAAAACCGAAAAAGTGTCTTTTA	2448
Db	1828	AACAATGTGGCGGATATAAACAATTCTGTAGATATATACACGTTGACATATAGACGAA	1887
Qy	2449	GATCGGAAAAAGAAATTTGTTAA	2471
Db	1888	CGGAGAAAAAACCAATCTTGA	1910

Search completed: July 30, 2004, 02:04:10  
Job time : 190 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 14:59:18 ; Search time 960 seconds  
(without alignments)  
11005.488 Million cell updates/sec

Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTTACAGAACCTTGAAGA 2487

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N Geneseq 29Jan04:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
  - 5: Geneseqn2001bs:\*
  - 6: Geneseqn2002s:\*
  - 7: Geneseqn2003as:\*
  - 8: Geneseqn2003bs:\*
  - 9: Geneseqn2003cs:\*
  - 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2485	99.9	2487	2 AAX20298	Aax20298 Borrelia
2	1083	43.5	1083	2 AAX61815	Aax61815 B. burgdo
3	979	39.4	979	2 AAX61816	Aax61816 B. burgdo
C 4	917.2	36.9	35515	2 AAX20252	Aax20252 Borrelia
C 5	827.4	33.3	2892	2 AAX20292	Aax20292 Borrelia
C 6	784	31.5	3129	2 AAX20285	Aax20285 Borrelia
C 7	733.8	31.5	5805	2 AAX20268	Aax20268 Borrelia
C 8	658.2	26.5	3653	2 AAX20280	Aax20280 Borrelia
C 9	493	19.8	2532	2 AAX20295	Aax20295 Borrelia
10	415.4	16.7	521	2 AAX20398	Aax20398 Borrelia
11	394.6	15.9	1047	2 AAX61805	Aax61805 B. burgdo
12	389	15.6	979	2 AAX61806	Aax61806 B. burgdo
13	385.4	15.5	1039	2 AAX61812	Aax61812 B. burgdo
14	385.4	15.5	1125	2 AAX61811	Aax61811 B. burgdo
C 15	336.8	13.5	9542	2 AAX20260	Aax20260 Borrelia
16	229.2	9.2	780	2 AAT10840	Aat10840 B. burgdo
17	137.4	7.9	1498	2 AAX83837	Aax83837 B. burgdo
18	188.8	7.6	1686	2 AAX87587	Aax87587 DNA encod
19	185.8	7.5	3399	2 AAT05868	Aat05868 Chicken l
C 20	175.6	7.1	6668	6 ABL33697	Ab133697 Human imm
C 21	173.6	7.0	6644	2 AAX33181	Aax33181 Base sequ
22	173.6	7.0	7372	2 AAX33182	Aax33182 Base sequ
23	173.6	7.0	7797	2 AAX33180	Aax33180 Cowpox vi

24	173.6	7.0	7996	2 AAX33184	Aax33184 Base sequ
25	161.8	6.5	3579	3 AAA70099	Aaa70099 Plasmodiu
C 26	161.2	6.5	6292	4 AAS46735	Aas46735 Tumour su
C 27	154.2	6.2	14005	6 ABL33958	Ab133958 Human imm
C 28	153.2	6.2	3683	7 ABZ10199	Abz10199 Haematopo
C 29	151.2	6.1	1998	3 AAA70212	Aaa70212 Plasmodiu
C 30	150.2	6.0	7442	4 AAS46686	Aas46686 Tumour su
C 31	147	5.9	6767	4 AAS46608	Aas46608 Tumour su
C 32	146.4	5.9	8056	7 ABZ10246	Abz10246 Haematopo
C 33	145.6	5.9	3683	7 ABZ10053	Abz10053 Haematopo
C 34	144.2	5.8	9539	4 AAS45347	Aas45347 Chemicall
C 35	144.2	5.8	9539	6 ABK28180	Abk28180 DNA trans
C 36	144	5.8	6334	6 ABL33213	Ab133213 Human imm
C 37	143.6	5.8	975	6 ABQ29508	Abq29508 Oligonuc
C 38	143.6	5.8	975	6 ABQ29509	Abq29509 Oligonuc
C 39	142.8	5.7	700	7 ACD92384	Acd92384 Human col
C 40	142.4	5.7	875	4 AAI95044	Aai95044 Human neu
C 41	141.2	5.7	34769	4 AAS45774	Aas45774 Tumour su
C 42	141	5.7	8079	6 ABL92313	Ab192313 Chemicall
C 43	140.4	5.6	8056	7 ABZ10246	Abz10246 Haematopo
C 44	139.8	5.6	529	7 ABX52180	Abx52180 Bovine ES
C 45	139.8	5.6	16033	6 ABL33404	Ab133404 Human imm

ALIGNMENTS

RESULT 1  
AAX20298  
ID AAX20298 standard; DNA; 2487 BP.  
XX  
AC AAX20298;  
XX  
DT 04-MAY-1999 (first entry)  
XX  
DE Borrelia burgdorferi polynucleotide sequence #51.  
XX  
KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
KW infection; diagnosis; characterisation; detection; ds.  
XX  
OS Borrelia burgdorferi.  
XX  
EN WO95858943-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 18-JUN-1998; 98WO-US012764.  
XX  
PR 20-JUN-1997; 97US-0050359P.  
PR 22-JUL-1997; 97US-0053344P.  
PR 22-JUL-1997; 97US-0053377P.  
PR 03-SEP-1997; 97US-0057483P.  
XX  
(HUMA-) HUMAN GENOME SCI INC.  
(MEDI-) MEDIMMUNE INC.  
XX  
PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
PI Smith HO;  
XX  
WPI; 1999-081217/07.  
XX  
New isolated Borrelia burgdorferi nucleic acids - used to develop  
PT products for the detection, diagnosis, characterisation, prevention and  
PT therapy of infections, particularly Lyme disease.  
XX  
PS Claim 1; Page 1028-1029; 1128pp; English.  
CC  
AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
CC detection, diagnosis, characterisation, prevention and therapy of Bb  
CC infections, e.g. Lyme disease. They can also be used for the production  
CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of

CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX  
SQ Sequence 2487 BP; 1021 A; 241 C; 453 G; 770 T; 0 U; 2 Other;

Query Match 99.9%; Score 2485; DB 2; Length 2487;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 CTTCGTAGTGTGAACAAATTTCTCTAATACAGTTACATTTCTTTTGTGCTGCTTTTTC 240

QY 241 CTTTATGTTGTATAAGTTTTCATTTTGTCTTAAAGTTGAAATATCTTGTGATTT 300  
DB 241 CTTTATGTTGTATAAGTTTTCATTTTGTCTTAAAGTTGAAATATCTTGTGATTT 300

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DB 841 GTATGTTTGTAGTCTTTTATTAATGACAGGCCATTTGCAATGGAGAGATTTTAGGGA 900

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QY 1081 GTTCTTGCAAGATTTGATGCAACTGTTAAAGATGCAACTGTTAAAGATGCAACTGTTAAAG 1140  
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DB 1201 AAGGATTTTAAAGATGTTTATGATCCAGTAAAGATTAATTTGCTTCAATTTGCTTCAAT 1260

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DB 1741 GGCCTGTATATGATTTATTTTACCGATGACAAACAAAAAGCTTATATATAAAGAGAGAG 1800

QY 1801 ATTTAGAGAGATTAAG 1860  
DB 1801 ATTTAGAGAGATTAAG 1860

QY 1861 GAGATGATTTAAG 1920  
DB 1861 GAGATGATTTAAG 1920

QY 1921 AGCCTCCTCTAAAG 1980  
DB 1921 AGCCTCCTCTAAAG 1980

QY 1981 AATCAGAGATTTAG 2040  
DB 1981 AATCAGAGATTTAG 2040











Db 2172 CCGGGCATTGTCAAATGGAGAGATTTTGGGAGTTGGTTAAATTTACATTGTGATTTGTT 2113  
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Db 2052 TTAGCTGTGTGTATGATTAGGACTTATGGAGAAATTTATGAATAGAAAAATGAAAAATG 1993  
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Db 1992 TTTATTTGTCTGTATTTTACTTTATAGTGTCTTGCATAATTTCAATCTCATATGAT 1933  
Qy 1110 GATGCAACTGGT----- 1121  
Db 1932 GAGCAAAAGTAGTGTGATGAGATAAACCATATTTTATATGATGAGCAAAAGTAATGAGTTA 1873  
Qy 1122 ----- 1121  
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Qy 1122 ----- AAAGATGCAACTGGTAAAGATGCA 1145  
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Qy 1146 ACTGCTAAAG----- 1156  
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Qy 1157 ----- 1156  
Db 1692 AACTTTTAAAAAAGCAATGACTAAAGCGGATCATTTAAACCTAGTTTGTATTATGATAT 1633  
Qy 1157 ----- 1156  
Db 1632 AAGTACGAACAAAGTAGTCAAAATGGTATCCAAAACAAAGAGATCATATAACAAAAATAGAA 1573  
Qy 1157 ----- 1156  
Db 1572 AGTATTANTGGTCTGACACATATTGCGTTTTHAGGAGATAAAATTAATACCGTGTGGG 1513  
Qy 1157 ----- 1156  
Db 1512 GGAGATAAAACAGCTGAATATGCAATACCACTAGAAAGTGTAAAAAAAATTTAAAAATAG 1453  
Qy 1157 ----- 1156  
Db 1452 AATTTAGAAATATAGGAGAGATAATATGCAATAAAAAACAATTTGATTTTGTGCTGTT 1393  
Qy 1157 ----- TGCAACTGGTAAAAATGCAGAACAAAAATA 1187  
Db 1392 TTTGCGCTGATAATTTCTTGCAGAAATTTTGCACACTGGTAAAGATATAAAACAAATTTCA 1333  
Qy 1188 AAGGGAAGTTCAAGATTTTGAAGAAATTTAGATCCAGTAAAGGATAAAATTTGCT 1247  
Db 1332 GAAGGGAAAAATTAAGGATTTGTAATAAGATTTTAGATCCAGTAAAGGATAAAATTTGCT 1273  
Qy 1248 TCAATAGTCCATAGCAGATGAATTTGGCAAAAAATTTACAAGAACGAAAAAGGTAAAT 1307  
Db 1272 TCAAGTGTACAAAAGTAGTAGTAGCAGCAAAAAATTTACAAGAACGAAAAAGAGAA 1213  
Qy 1308 AACGGGAAGAAG----- 1320  
Db 1212 TTAATGCGGGCGATGATCCTAATGGCAGTGGGAATAAATCCGCCACAGTATTGCCGGAA 1153  
Qy 1321 ----- AAAATGATAAGCTGTCTTTTGGAGAGAGATCAAAAGAGATCAAGAGAA 1373  
Db 1152 AATATTCAATTAATGCAATTAGTTTAAAGCAATTAAGAACAAAGTATGCTCACAAGAA 1093  
Qy 1374 AATGAGCAA-----GCTGTATTTAGAGAAAAAATCGCGAAGAGGATAAGAA 1424  
Db 1092 AAAAAAGTAGAAGAGCTGAAGCTAAAGTTGAAGAAAAATAAGAAAAAACAAGAGATAACA 1033

RESULT 6  
AAX20285/c  
ID AAX20285 standard; DNA; 3129 BP.

Qy 1425 GTTGTAAATTTAGAGAGAAAAAATTAAGAGTTAAAAAAGAGACTGAAGAGATGAAGAT 1484  
Db 1032 GAAGAAACATTTAAGAAARAGAAATATAGACGAACAAAACAACAAAGATTTAGCTAAA 973  
Qy 1485 AAAGAGAAATTAGAGAAACAAAAACAAGAACTGGAAAGACACAAAGAAAGAAAAACAAGA 1544  
Db 972 GCTAAGAGAGAGAAACACAAAAAAAGACAAAAAAGACATCAAGAGAGACAAACAAGAAA 913  
Qy 1545 CAAGAGAAAAAGAAACGAAAAAACAAGAACAGCAAGAGAAAAAAGAAACGAAAAACGACAA 1604  
Db 912 GCTAAGACAGAAAAAAGAAAAAGAGAAAGAGCGCAGAACAAACAAACGACACAA 853  
Qy 1605 GAACAAAGAAAGAAAGAGAGCTAAAAACAAAATTTAAAAACCTTGGCGATAAAATAGAT 1664  
Db 852 GAAGAGGAGAAAAAAGGCAAGTTGATAACCAAAATTTAAAAACATTTATAGCTAAAAATAGAT 793  
Qy 1665 GAGATAAGTTGGAATATTGATGTTAGAAAGTCAAAACAGTGTAAACCGGAAACGAGAGCTT 1724  
Db 792 GAGATCAATGAATATTGATGTTTAAATGGCAACGACTGTAGGCCCAAGAGCGTT 733  
Qy 1725 ATAGATAAAATTAACGGGCTGTATATGATTTATTTTACCGATGACAAACAAAAAGCTATA 1784  
Db 732 ATAGATAAAATTAACGGGCTGTATGATGATTTTACCAATGGCAATTAATCTTATACGC 673  
Qy 1785 TATAAACAATCGGAGATTTAGAGATCAAGACGCGAGGATTTGGGAAAAATTTTGNAA 1844  
Db 672 GAACTTGGGAGGCTTAGAAGAGGAATCAGAACGAGGATTTAGGAAAAATTTTGNAA 613  
Qy 1845 GAACTTGGATGATCTAGAGATGAGTTAAGAACCAAAATTTAAATAAGATAATATAAAAAATAT 1904  
Db 612 GAACTTGGATGATCTAGGACGCGCTAAGAACTAAATTTAAATGAAGCAATAACCATAT 553  
Qy 1905 TATGCCCATGAAATAGAGCTTCTCTAAAGAAAAATGTAGATGTACGCGAAATTTAAAGAA 1964  
Db 552 ACTGGTTACGAA--GAGCCTAAGTTAAAGAAAGTGTAAATGTTAGCGAAATTTAAAGAA 496  
Qy 1965 GATTTAGAAAAAGTAAATCAGGATTTAGAAAGGTTTAAAGAAATCTTTAAAGACAAATCT 2024  
Db 495 GATTTAGAAAAATTAATTAATTAATTAAGAGAGTTTAAAAAAATCTTTAAAGATAGTTCT 436  
Qy 2025 AAATTTGAAGAAATTTAAAGGATACATCAGTTACAGTCAAGTAAATTTATTTGATCTTTTA 2084  
Db 435 AAATTTGAAGAAATTTAAAGGATACATCAGTCACAGTCAAGTAAATTTATTTGATGCTTTA 376  
Qy 2085 GATGTAACTAAATTTTACGTACACAAAATACACAGTACAGTAAAGTTTCACTGGCTGTTA 2144  
Db 375 GGTGTAACTAAA-TTTCGCTATACAAAGTACACAGTACAGTAAAGTTTCACTGGCTGTTA 317  
Qy 2145 TTTTTTTGTAGATTTCAATTTGTATGAATATAGAAATGTTTTCTATCAAACTTTCAITTA 2204  
Db 316 TTTTTTTGTAGATTTCAATTTGTATGAATATAGAAATGTTTTCTATCAAACTTTCAITTA 257  
Qy 2205 AAAAGTG-CAAAAACATTTGCTAAAAATGTTGTTTTTATATCTCTAGAGCTATGA 2263  
Db 256 AAAAATGCCAAAACTATGCTCAAAAATTTGTTTTTATATCTATCTATATAATTAATA 197  
Qy 2264 CGTATACAAATGAGATTTCAAGTTTTCAGTATAATTTATATAAGAAAAACAAAAAGAAA 2323  
Db 196 TGCATCTAATGAATTTCAANTTTTTATGATATCTTAGTGAGATTTAAAAAAGTCAA 137  
Qy 2324 TAGATAAATTTATAACAAGCTCTATTATACTAGCCNAAATAACTCTTAAAGCAAAAAAGAC 2383  
Db 136 TAAATAAACTT-----TATGAAACCGGAAACAAAGCAACCGCAAGAACAAAAAGTC 89  
Qy 2384 AAATNTACAGTGTGTTGAAGAGATGCAAAATACGTAATAAAAAACCGGAAAAAG 2438  
Db 88 AAATGTATAGCTCTTATTAAGCAGCGCAAGATACGGAATAAAAAACTGGAAAAAG 34

XX AAX20285;  
AC  
XX  
DT 04-MAY-1999 (first entry)  
XX  
DE Borrelia burgdorferi polynucleotide sequence #38.  
XX  
XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
KW infection; diagnosis; characterisation; detection; ds.  
XX  
XX OS Borrelia burgdorferi.  
XX  
XX WO9858943-A1.  
XX  
XX 30-DEC-1998.  
XX  
XX 18-JUN-1998; 98WO-US012764.  
XX  
XX 20-JUN-1997; 97US-0050359P.  
XX  
XX 22-JUL-1997; 97US-0053344P.  
XX  
XX 22-JUL-1997; 97US-0053377P.  
XX  
XX 03-SEP-1997; 97US-0057483P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX (MEDI-) MEDIMUNE INC.  
XX  
XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
PI Smith HO;  
PI  
XX WPI; 1999-081217/07.  
XX  
XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
PT products for the detection, diagnosis, characterisation, prevention and  
PT therapy of infections, particularly Lyme disease.  
XX  
XX Claim 1; Page 1004-1006; 1128pp; English.  
XX  
XX AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
CC detection, diagnosis, characterisation, prevention and therapy of Bb  
CC infections, e.g. Lyme disease. They can also be used for the production  
CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX  
XX Sequence 3129 BP; 1067 A; 566 G; 286 G; 1210 T; 0 U; 0 Other;  
Query Match 31.5%; Score 784; DB 2; Length 3129;  
Best Local Similarity 64.9%; Pred. No. 3.8e-96;  
Matches 1272; Conservative 0; Mismatches 650; Indels 38; Gaps 6;  
94 TGAATTTTCAAAAATAAGTAGCTCTGTATCAAGATTTTCTCAATTAAGATTTT 153  
3129 TGTCTTTTGGAAAGATAGTAGCGCTTGAGTCAAGAGTTTCTTGGAAATGATTTT 3070  
154 TGTGTGCTGTTCGATAGCTCGAATCTTCTGAGTTGATACAAATTTCTTAATACAAG 213  
3069 TATGTGCTGTTCGATAGCTCGAATCTTCTGAGTTGATGACATTTCTTAATACAAG 3010  
214 TTACATTTCTTTTTTGGCAGATTTACATTTTATGTTGATATAAGTTTTCATTTTGC 273  
3009 AGGTATTTCTTTTTTGGCAGATTTTACTTTTATAGTATATAAGTTTTCGGGTTTGC 2950  
274 TTAATAAAGTTTGAATATCTTGATTTTACTTTTTTTCAGTTTCGGTGCCCTGCGAGCCAC 333  
2949 TTAATAAAGTTTGAATATCTTGATTTTACTTTTTTTCATTTTTCAGTGCCTCTACATCCAC 2890  
334 TTATTCGAGTAAATGTAAACCAACCAAGATTTGATTCAGCTTGTGTTAAAGATTTTGA 393  
2889 TTATTAAGAGTAGATGCACAAACCAACCAAGATTTGGGTCAATTTGTTTAAAGGTTTGG 2830

QY 394 TGCATTTTCAATAGTTTGGCCAAATTTTGGGGTCAAAATTAATAATTTAGAGTTGGCTTTG 453  
DB 2829 CACATTTTACAAATTAATTTAATACCTTTTAGGGGTAAATAAACTTAGGAGTTGGTTTG 2770  
QY 454 AAGCTTTTGTAGGCTTAGAAGAAATTTTATAGTGAATTTTAAAGAAATTTTGTTCAT 513  
DB 2769 AATTTCTTTTACCTTTAGATGAATTTTATAGTGAATTTTAAAGAAATTTTGTTCAT 2710  
QY 514 TTATAGTTTTCATGATCTTGAATAATTAAGCATAAATCTATGTTGAATTTTAA 573  
DB 2709 TTATAGTTTTCATGATCTTGAATAATTAAGCATAAATCTATGTTGAATTTTAA 2650  
QY 574 AATTAAGATTAATTTATGTCATTAATAATCCCTCTTATAGTCTTACTTTTAAATTA 633  
DB 2649 AATTAAGATTAATTTATGTCATTAATAATCCCTCTTATAGTCTTACTTTTAAATTA 2590  
QY 634 AGTAAAGATTAATAAATTTGATTAATAATTTATATTTTACCAAAAACAAAAAAT 693  
DB 2589 AGTAAAGATTAATAAATTTGATTAATAATTTATATTTTACCAAAAACAAAAAAT 2530  
QY 694 TTAGTCAAAATTTGTGGCTTCTCATGTCATGCAAAATTTGGATTTAGGATCTGAT 753  
DB 2529 TTAGTCAAAATTTGTGGCTTCTCATGTCATGCAAAATTTGGATTTAGGATCTGAT 2470  
QY 754 AACAGAAAGAGGCAATTTTAAAGGGTGCACCTTAAGAAAGATTAATCTATGTTAAAGTGA 813  
DB 2469 AACAGAAAGAGGCAATTTTAAAGGGTGCACCTTAAGAAAGATTAATCTATGTTAAAGTGA 2410  
QY 814 TATAGCAAAAGATTTGAAATTTAAGTTGATGTTTGTAGTCTTTTATATAGGACAG 873  
DB 2409 TATAGCAAAAGATTTGAAATTTAAGTTGATGTTTGTAGTCTTTTATATAGGACAG 2351  
QY 874 CCATTTCCAAATTTGAGAGATTTTAAAGGGTGCACCTTAAGAAAGATTAATCTATGTTAAAGTGA 933  
DB 2350 CCATTTCCAAATTTGAGAGATTTTAAAGGGTGCACCTTAAGAAAGATTAATCTATGTTAAAGTGA 2291  
QY 934 TGTAAATAGCTGAATTTAAACAAATTTATATTTTAAATCTTTTGAATAATTTGATTTG 993  
DB 2290 TGTAAATAGCTGAATTTAAACAAATTTATATTTTAAATCTTTTGAATAATTTGATTTG 2231  
QY 994 GGGTTGGTAAACTTAAGGCTTTTAAAGGGTGCACCTTAAGAAAGATTAATCTATGTTAAAGTGA 1052  
DB 2230 GTGTTGGTAAATTTAAGTGAATTTTAAAGGGTGCACCTTAAGAAAGATTAATCTATGTTAAAGTGA 2171  
QY 1053 ATTATTTGTGCTGATTTTGTGCTGATTAAGTTTCTTGAAGATTTGATGCAACTGTTAAAGTGA 1112  
DB 2170 ATTATTTGTGCTGATTTTGTGCTGATTAAGTTTCTTGAAGATTTGATGCAACTGTTAAAGTGA 2111  
QY 1113 GCAACTGTTAAAGATGCAACTGTTAAAGATGCAACTGTTAAAGATGCAACTGTTAAAGTGA 1172  
DB 2110 TTAAGAC---AAATGTTAAAGAAAGATTTGAAAGATTTTATAGTAAAGATTTAAAGTGA 2054  
QY 1173 GCAGAACAAATATAAAGGGAAAGTTTCAAGGATTTTAAAGAAAGATTTTAAAGTGA 1232  
DB 2053 GGTGACCATCTTAATACAGTCTGTTTAAATCCACCAGTATTTGCGGCAAGTTCCAC 1994  
QY 1233 AAGATTAATTTGCTTCAATGTTCCAAATGAGTGAATTTGCGCAAAATTTTAAAGTGA 1292  
DB 1993 GATAACACACCCGTTTAAAGGGGTTTCAAGGATTTTAAAGAAAGATTTGTTGTTCAAGTGA 1934  
QY 1293 GAAGAAAGGTTAAATTAACGGGGAAGAAATTTGATAAGTCTGCTTTTAAAGTGA 1352  
DB 1933 GAAGAAAGGTTAAATTAACGGGGAAGAAATTTGATAAGTCTGCTTTTAAAGTGA 1874  
QY 1353 TCAAAAGG-----ATGAAGAAAGAAATTTGAGCAAGCTGTTAAATTTAGAGTGA 1400  
DB 1873 TTAAGAGGCTAGAAAGAAATTTTCAAGATTTTAAAGAAATTTTAAAGTGA 1814  
QY 1401 AAAATTCGGGAGGAGGATTAAGAGTGTAAATTTTAAAGAGAGAAATTTAGAGTGA 1460  
DB 1813 GAAAGTCTGAGAAAGTTTAAAGAAATTTTAAAGAGAGAAATTTTAAAGTGA 1754  
QY 1461 AAAGAGACTGAAGAGTGAAGTAAAGAAAGAAATTTAGAGAAACAAAAACAAAGTGA 1520

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Db 1753 AAAGATTGGGTGTAATGGAGTTATCTCTTAATGATGCTACTAATACTAATGATTTT 1694
Oy 1521 AAACACAAAGAAACAAACACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1580
Db 1693 GTAAAAAGGTTATAGATGATGCTCTTAAATAATATTGAGGAAGAACTTGAAGCTAGCA 1634
Oy 1581 GAAGAAAGAAACGAGACGACAGACAGACAGACAGACAGACAGACAGACAGACAGAAATT 1640
Db 1633 GAGCCTCAAAATATAGAGAGATAGAGAGATAGAGAGATAGAGAGATAGAGAGATAGAT 1574
Oy 1641 AAAAATCTTGGGATATAATAGATGAGATAGATAGATAGATAGATAGATAGATAGATAGAT 1700
Db 1573 AAACACAAAGACTACATGATGCTTATGTTTATTAGCATTTACATTTGCTGAAATTAG 1514
Oy 1701 ACAAGTGAACACGAGACGCTTATAGATAGATAGATAGATAGATAGATAGATAGATAGAT 1760
Db 1513 GCNA---TAAAGCTAGGAGGGGATATGAAAAAATTAGTCTGTTAATATTTTGTGTTT- 1458
Oy 1761 ACCGATGACACAAAAAGCTATATATAAAACATGGGGAGATTTAGAGATGAGAGGC 1820
Db 1457 -----ATTGTAGTAAGTTTAAAGTCAAAATATAGAGAGAAATTATACA 1415
Oy 1821 GAAGATTGGGAAATATTGAAAGAAATGAGTGATAGATAGATAGATAGATAGATAGATAGAT 1880
Db 1414 GAAACTAAAGAGCTTTTCTAAAGAGAGATTTAAACCTAATAATAAAGACCTAGATAAT 1355
Oy 1881 TTAATAAGATATAAAATATATTATGCCATGAGAAATGAGCTCTCTTAAAGAAAT 1940
Db 1354 TATGATTTAAATGAGTATGAAAAAGTCAITGTTTTTCCGATGCTCTAGAAATTAGA 1295
Oy 1941 GTAGATCTCAGCGAAATTAAGAGAGATTTAGAAAAAGTAAATCAGGATTAGAAAAAGGTT 2000
Db 1294 GGAGATTAAAGAAAAATGGAATTTAAAGAAAAAGTGTTTTTTGGACGCTCTTGAGGCT 1235
Oy 2001 AAAGAAATCTTAAAGACAAATCTAAATTTGAAGAAATTA 2040
Db 1234 ATTGAATCTCTTAAAAAATTAAGATAAGTACTGATAGTA 1195

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## RESULT 7

AAAX20268/c

ID AX20268 standard; DNA; 5805 BP.

XX AC AX20268;

XX DT 04-MAY-1999 (first entry)

XX DE Borrelia burgdorferi polynucleotide sequence #21.

XX KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
 XX KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
 XX KW infection; diagnosis; characterisation; detection; ds.

XX OS Borrelia burgdorferi.

XX PN W09858943-A1.

XX PD 30-DEC-1998.

XX PF 18-JUN-1998; 98WO-US012764.

XX PR 20-JUN-1997; 97US-0050359P.

XX PR 22-JUL-1997; 97US-0053344P.

XX PR 03-SEP-1997; 97US-005377P.

XX PR 03-SEP-1997; 97US-0057483P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (MEDI-) MEDIMUNE INC.

XX PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;

XX PI Smith HO;

XX

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DR WPI; 1999-081217/07.
XX New isolated Borrelia burgdorferi nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention and
PT therapy of infections, particularly Lyme disease.
XX Claim 1; Page 959-962; 1128pp; English.
XX AAX20248 to AAX20402 represent polynucleotide sequences isolated from
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the
CC detection, diagnosis, characterisation, prevention and therapy of Bb
CC infections, e.g. Lyme disease. They can also be used for the production
CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of
CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing
CC fever, and Lyme borreliosis, more commonly known as Lyme disease
XX Sequence 5805 BP; 1878 A; 1000 C; 614 G; 2290 T; 0 U; 23 Other;
SQ
Query Match 31.5%; Score 783.8; DB 2; Length 5805;
Best Local Similarity 82.9%; Pred. No. 4e-96;
Matches 926; Conservative 0; Mismatches 172; Indels 19; Gaps 2;
Oy 1 ATTTATTTACACGAAACCTGACTTTTGGAGAGATTTTGAATTTATTAGAAATATGGA 60
Db 4964 ATTTATTTACAGAAATCCGATTTTAAAGAGATTTTGAATTTTGAATATATGGA 4905
Oy 61 TTAATGCTAATTTGGTGTCTTTAAACCTTAATGTTTGAATTTTGAATAAATAAGTACGTC 120
Db 4904 CAATATCAATTTGGTGTATCTTTAAACCTTATGTTTCTTTTGAATAAATAAGTACGTC 4845
Oy 121 TTGTTATCAAGATTTTCTCATTAATAATGATTTTCTGTGCTGTTTGGATAGCTCGAAT 180
Db 4844 GCGAGTCAAGAGTTTCTTGGAAATGATTTTAAAGTGTGTTTGGATAGCTCGAAT 4785
Oy 181 CTCTGAGTGTATAACAATTTCTCTAATACAAAGTTTACATTTCTTTTGGCACATTTA 240
Db 4784 CTCTGAGTGTATGATCAATTTCTCTAATACAAAGGTTATTTCTTTTGGCACATTTA 4725
Oy 241 CTTTATGTTGTATAAAGTTTCTTCAATTTTGCCTTAAAAAGTTGAATATCTTGCATTT 300
Db 4724 CTTTAATAGTATATAAAGTTTCTCGGTTTTCGTTTAAAAAAGTTGAATATCTTGCATTT 4665
Oy 301 TTACTTTTTCAGATTCGGTGGCCCTGCGAGCACTTTATTCGAGTAAATGTAAAAACCAAC 360
Db 4664 TTACTTTTTCGATTTTCAGTGGCTCTACATCCATTTAAGAGTAGATGCACAAACCAAC 4605
Oy 361 CAGATATTGGATCAGCTTGTTTAAGAGTTTGTATGTCATTTTCAATTTAGTTTGCATTT 420
Db 4604 CAGAAATTTGGTCAATTTGTTTGGGTTTGGCACATTTTGAATTAATTAATACATTT 4545
Oy 421 TTGGGGTCAAAATAAAAATTTAGAGTTGGCTTTGAAGCTTTTGTAGTAGCTTAGAAGAA 480
Db 4544 TAGGGGTCAATAAAACTTAGAGTTGGTGTGTTTGAATTTTCTTACGTTTAGTGAAT 4485
Oy 481 TTTTATAGTA-----ATTTTAAAGAAATTTGTTTTCATTTATTTAGTT 522
Db 4484 TTTCTAGAGATTTAAGAAATTTTATTTCTAGAAATTTGTTTATTTAATGCAT 4425
Oy 523 TTTGATGATCTGTATAAATTTAGCATAAATCTATGTTGAAATTTTAAATTAAGAT 582
Db 4424 TTTGATGATCTGTATAAATTTAGCATAAATCTATGTTGAAATTTTAAATTAAGAT 4365
Oy 583 AATTATTTCATGCCATAAAATCCCTCTCTTATAAGTGTACTTTTAAATTAAGTAAAGT 642
Db 4364 AATTATTTCATGCCATAAAGCTCTCTTATAAGTGTACTTTTAAATTAAGTAAAGT 4305
Oy 643 AATAAATAATGATTAATAATGATTTATTTATTTTACCAAAACAAAAAATTTAGTCAA 702
Db 4304 AATAAATAATGATTAATAATGATTTATTTATTTTACCAAAACAAAAAATTTAGTCAA 4245
Oy 703 TTGTGTGCTTCTCATTTGCATGCAAAATTTGGAATTTAGGATAGCTGTATGATAACAGAG 762

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4244	Db	TTTTGTGAGTTCTCATTGCAATGCAAAATCTGGGCTGTAGACGAGGTGGGATAAACAGAAG	4185
763	Qy	AGGCAATTTTTTAAGGGGTGCACCTAAGAAAGATACTACTTTTAAAGTGATATATAGCAAA	822
4184	Db	AGGCATTTTTTAAGGGGTGATACACAGAAGATACATATCTTGTGTAAATATATAGCAAA	4125
823	Qy	GACTTTGAAATTTAAAGTTGTATGTGTTTTGTAGTCTTTTATAATGACAGCCCATTTGCA	882
4124	Db	GACTTTGAAATTTAAATTTGTATGTGTTTTGTAGTCTCTTATAATGAGTAGTGCAATTGCA	4065
883	Qy	ATGAGAGATTTTAGGAGATTGATTAATAATATATTTGCGTTTGTGTTTAAATATGTAATAGC	942
4064	Db	ATGAGAGATTTTATGATGTTTATGATTAATAATTACATTTTAGTTTTGTAAACAATGTAAAT-TC	4006
943	Qy	TGAATGTACAAAAATTATATATTTAAATCTTTGAAAAATTGTAATCTGTTGGGTTCTGG	1002
4005	Db	GAAATGTACAAAAATTATATTTAAATCTTTGAAATATTGCAATTTATTGCTGTTGTTGG	3946
1003	Qy	TAAACTTTAAGCCTTATCGAGTGGATTATGAATAAAAAAATGAAAAATTTTATTATTGTTG	1062
3945	Db	TAATATTGGGACCTATGAGTAAGTCTTATGAATGAATAAGAAAAATTTTAAATTATTGTTG	3886
1063	Qy	CTGTATTGTGCTGATAAGTTCTTTCGAAGATTGTATGC	1099
3885	Db	CAGTTTTTGTTCATTAATTTCTGTAAAAATAATAC	3849

RESULT 8  
AAX20280

AA20280  
ID AAX20280 standard; DNA; 3653 BP.

XX AAX20280:

04-MAY-1999 (first entry)

XX DE *Borrelia burgdorferi* polynucleotide sequence #33.

XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
KW infection; diagnosis; characterisation; detection; ds.

OS *Borrelia burgdorferi*.

XX PN WO9858943-A1.

XX PD 30-DEC-1998.

XX  
PF 18-JUN-1998: 98WO-US012764.

XX  
20-JUN-1997: 97US-0050359P.

PR 20-JUN-1997; 97US-0050359P:  
PR 22-JUL-1997: 97US-0053344P:

PR 22-JUL-1997; 97US-0053377P.  
PR 22-JUL-1997; 97US-0053377P.

PR 03-SEP-1997; 97US-0057483P.  
PR 03-SEP-1997; 97US-0057483P.  
PR 03-SEP-1997; 97US-0057483P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMMUNE INC.

AA  
PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;

PI Label C,  
PI Smith HO;

WPI: 1999-081217/07.

AA New isolated *Borrelia burgdorferi* nucleic acids - used to develop  
PT products for the detection, diagnosis, characterisation, prevention and  
PT therapy of infections, particularly Lyme disease.  
PT

XX  
PS  
Claim 1: Page 994-996; 1128pp; English.

AXX20248 to AAX20402 represent polynucleotide sequences isolated from *Borrelia burgdorferi* (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. *Borrelia* belongs to a family of

CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX  
SO Sequence 3653 BP; 1587 A; 348 C; 690 G; 1027 T; 0 U; 1 Other;

Query Match 26.5%; Score 658.2; DB 2; Length 3653;  
Best Local Similarity 70.8%; Pred. No. 2.3e-79;  
Matches 967; Conservative 0; Mismatches 370; Indels 28;

1138	Qy	AA	GATGCA	ACTGGT	TAAGATG	CAACTGGT	TAAGAAATGC	AGACACAAAATAT	ATAAAGGGAAG	1139
1216	Db	AA	GAAGATA	AAAAATAA	AGGGGTG	TAGAAGAAACAAT	TAAGATGAATTAAT	GCAGGGTGATG	1217	
1198	Qy	TT	CAAGGAT	TTTTAG	AAAAAGATTTAG	ATCCAGT	TAAGAGATAAAAT	TGCTTCAAAATGGTC	1199	
1276	Db	AT	CCTAAT	ACTGGT	TGTAATAAATTCGT	CACAGTATTG	CCAGAAAAATAGT	CAAGATAATA	1275	
1258	Qy	CA	ATAGCAG	ATGAAT	TGGCAAAAAAT	TACAAGAGNAG	AAAGGTAAATAAC	CGGGAAG	1257	
1336	Db	CA	CAATAT	TTAAAG	CGACGGCA	CAAAAGTGGT	CAACAGAGAG	AGAAAGTGA	1335	
1318	Qy	AAG	AAAATG	ATAAG	CTGCTCTTTTAG	GCAAGAATCAAA	AGAGGATGCA	AGACAAAAATG	1317	
1396	Db	TAG	NAGAT	CCGAG	CTTAAGTTGAG	GGAATAAGAGAAAA	CAAGAGATAC	AGACAAAC	1395	
1378	Qy	AG	CAGCTG	TTAATTTAG	AGAAAAAATTCG	GAGAGGATAG	AAAGTTGTAATTTAG	1377		
1456	Db	GA	ACAAAC	AGATTTAG	CTTAACNAG	AGAGAACCAACAAAA	CGAAAAAGCAG	ACACAG	1455	
1438	Qy	AAG	AGAAAG	AAATAG	AGTTAAAAA	AGAGACTGAAG	AAAGTGAAGATAA	AGAGAAATAG	1437	
1516	Db	AA	AAACAA	AAAGAG	AGAGAGCAG	AGAGACAA	AAAAAGAGAGAG	CAAGAGAAAG	1515	
1498	Qy	AG	AAACAA	AAACAG	AGTGGAAAA	ACACAGAA	AAAAACACGAC	AGAGAAAAAG	1497	
1576	Db	AA	AGCTA	AGG	CAGAAAAA	AGAGCTTAAG	AAAAAAGCAG	AAAGACAAAA	1575	
1558	Qy	AA	CGAAAA	AAACAG	AGACAGCA	AGAAAGAAAC	CGAACAGAA	CAAAAGAAAG	1557	
1636	Db	AA	AAACG	AAAG	CGAAAAA	AGAGAGAG	AGACAAACG	AGAGAGAGAG	1635	
1618	Qy	AA	GGAG	AGCT	TAAAA	CAAACTTGG	CGGATAAAATAG	ATGATGAGTAAGTTGG	1617	
1695	Db	-----	GTTG	ATAACG	AAATTTAG	ACACTTAC	GAGCAAAATAG	ATGAAATCAATGAA	1694	
1678	Qy	AT	TTGATG	GTATAG	AAAGTCAAA	CAAGTGTAA	AAACCGAAAGCAG	TTATAGATAAAATTA	1677	
1747	Db	AT	TTGATG	TTTAA	AGCCAACTAG	TGTGGGGC	CAAGGTGTTATAG	ATAGATAATTA	1746	
1738	Qy	CG	GGCCCTG	TATGAT	TATTTTAC	CGATGAC	AAACCAAAAGCT	TATATATAAATCATGGG	1737	
1807	Db	CAG	GGCTGT	ATATGAT	GATTTTACT	GTATG	-----CGAA	TAAAGCTTATAC	1806	
1798	Qy	GAG	ATTTAG	AGAGTGA	AGAGCGCAAG	GTGGGAAAAAT	TATTC	AAAGAAATTTGATGATTA	1797	
1864	Db	GG	GATTTGG	AGATGAT	TAACACG	AGAGATTAG	AGAAAGCTTATTA	AAAGAAATTTGATGATA	1863	
1858	Qy	CT	AGATG	AGT	TTAAGAC	CAAAATTTAA	ATTAAGATAATA	AAAAATA-----TTATGCC	1857	
1924	Db	CT	AGACAT	AAATTTA	AGAACCAAAATTA	ATAGGGGTAA	TAAAGCATATAT	TATTTGATATA	1923	
1912	Qy	AT	GA	AAATG	AGCTCTCT	TAAACAAAAAT	GTAGATGTCAG	CGGAATTTAAAGAGATTTAG	1911	
1984	Db	GA	GC	ACTG	AAACCCCAATTTAA	AGAAATG	TTAGTGT	TTAGCGAAATTTAAATCAG	1983	
1972	Qy	AAA	AGTAA	AAATCAG	AGTTAG	AAAGGTTAA	AGAAATCTCT	TAAAGACAAATTTCTAAATTTG	1971	
2044	Db	AT	GA	ACTAA	AAATCAAAAT	TTAGNAG	AGTTAAAGAAATCT	TTGAAGATAAAGATAAATTTG	2043	
2032	Qy	AA	GA	ATTTAA	AGGATAC	ATCAGTTAC	AGTCAG	-----TAA	TTATATTCGATGCTTTT	2031
2104	Db	AAG	AAATTTAA	AGATA	CTGCTCGT	GTAGGAGTA	ATATGAT	CGAAGATTAATTTT	2103	



QY 1399 AAAAAATGCGAAGAGGATAAGAAAGTCTGTTAATTTAGAGAGAAAGAAATTTAGAAAGTTA 1458  
 Db 1650 AAACATATCTGATTATGAAAGGAAATAGAGAATT--AAAGGAAAAAATCTAAAGAGATA 1594  
 QY 1459 AAAAAAGAGACTGAAGAGATGAAGATAAAGCAAGAAATAGAGAAACAAAAACAAGAGAGTGG 1518  
 Db 1593 AAGAAAGTTTGAAGAAAGATTAGAAATCCCTTGAGAAAGCTTTAAATGAAAAAATAGAGA 1534  
 QY 1519 AAAAAAGCAGCAAGAAAGAAAAACAAGCAAGAGAAA 1553  
 Db 1533 AAAAAAGAAAGAAATTAAGAGAGTCTCAAAAAAAA 1499

RESULT 10  
 AAX20398  
 ID AAX20398 standard; DNA; 521 BP.  
 AC AAX20398;  
 DT 04-MAY-1999 (first entry)  
 DE Borrelia burgdorferi polynucleotide sequence #151.  
 KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
 KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
 KW infection; diagnosis; characterisation; detection; ds.  
 XX Borrelia burgdorferi.  
 OS  
 XX WO9858943-A1.  
 FN  
 PD 30-DEC-1998.  
 PF 18-JUN-1998; 98WO-US012764.  
 PR 20-JUN-1997; 97US-0050359P.  
 PR 22-JUL-1997; 97US-0053344P.  
 PR 22-JUL-1997; 97US-0053377P.  
 PR 03-SEP-1997; 97US-0057483P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
 PI Smith HO;  
 XX WPI; 1999-081217/07.  
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
 PT products for the detection, diagnosis, characterisation, prevention and  
 PT therapy of infections, particularly Lyme disease.  
 XX  
 XX Claim 1; Page 1111-1112; 1128pp; English.  
 CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
 CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
 CC detection, diagnosis, characterisation, prevention and therapy of Bb  
 CC infections, e.g. Lyme disease. They can also be used for the production  
 CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
 CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
 CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
 CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
 XX  
 XX Sequence 521 BP; 182 A; 42 C; 93 G; 204 T; 0 U; 0 Other;  
 SQ

Query Match 16.7%; Score 415.4; DB 2; Length 521;  
 Best Local Similarity 87.3%; Pred. No. 6e-47;  
 Matches 455; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
 QY 446 TGGCTTTGAAGCTTTTATAGAGCTTGAAGAAATTTTATAGTGAATTTTAAAGATTTT 505  
 Db 1 TGGTTTGAAGCTTTTATAGAGCTTGAAGAAATTTTATAGTGAATTTTAAAGATTTT 60

QY 506 GTTTTCATTATTATAGTTTTCATGATCTTGTAAATAATTTAGCATATAAAATCTATGTTGAA 565  
 Db 61 ATTTTCATTATTAGCATTTTGTATATCTTGAATATCTTGAATATAGTTTGAATATCCATGTTGAA 120  
 QY 566 ATTTATTTAAATTAAGATAAATTTATTCATGTCATATAAAATCCCTCCCTTATTAAGTGTACTT 625  
 Db 121 ATTTATTTAAATTAAGATAAATTTATTTAGTGTTCATATAAAATCCCTCCCTTGAAGTGTACTT 180  
 QY 626 TTAATTTAAGTAAAGTAAATTAATAAATTTGATTAATAAATGTAATTTATATTTTACCAAAAC 685  
 Db 181 TTAATTTAAGTAAAGTAAATTAATAAATTTGATTAATAAATGTAATTTATATTTGACCAAAAC 240  
 QY 686 AAAAAAATTTAGTCAAAATTTGTGGCTTCTCATTCATTCGATGCAAAATTTGGATTGTAGGATA 745  
 Db 241 GAAAAAATTTAGTCAAAATTTGTGGCTTCTCATTCGATGCAAAATTTGGATTGTAGGAG 300  
 QY 746 GCTGTGATAAACAAGAGGCAATTTTAAAGGGTGCACTTAAAGAAAGATACTATCTTT 805  
 Db 301 GCTGTGATAAACAAGAGGCAATTTTCTGAGGGTGTGCGCTAAAGAAAGATACTATCTTT 360  
 QY 806 AAGTCATATATAGCAAAAGACTTTTGAAATTTAAGTTGTATGTTTGTAGTCTTTTATAA 865  
 Db 361 AGCTAATATATAGCAAAAGACTTTTGAAATTTAAGTTGTATGTTTGTAGTCTTTTATAA 420  
 QY 866 TGAGCAGGCCATTTGCAATGGAGAGATTTTGGAGGTGATTTAAATTTATTTGCGTTT 925  
 Db 421 TGAGTGTGCAATTTGCAATGGAGAGATTTTGGAGGTGATTTAAATTTATACATTTGCGTTT 480  
 QY 926 TGTAAATATGTAATAGTGTGATTAACAAATTTATATATTT 966  
 Db 481 TGTAAATATGTAACAGCTGATGTAACAAATTTATATATTT 521

## RESULT 11

AAX61805  
 ID AAX61805 standard; DNA; 1047 BP.  
 AC AAX61805;  
 DT 19-JUL-1999 (first entry)  
 DE B. burgdorferi antigenic protein coding sequence, f45-2.nt.  
 XX Antigenic protein; vaccine; Lyme disease; infection; detection; ss.  
 XX Borrelia burgdorferi.  
 OS  
 PN WO9859071-A1.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 18-JUN-1998; 98WO-US012718.  
 XX  
 PR 20-JUN-1997; 97US-0050359P.  
 PR 22-JUL-1997; 97US-0053344P.  
 PR 22-JUL-1997; 97US-0053377P.  
 PR 03-SEP-1997; 97US-0057483P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 XX Choi GH, Erwin AL, Hanson MS, Lathigra R;  
 PI  
 XX WPI; 1999-189980/16.  
 DR P-SDB; AAY20108.  
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
 PT products for the diagnosis, prevention and treatment of diseases caused  
 PT by Borrelia, particularly Lyme disease.  
 XX  
 XX Claim 1; Page 199; 275pp; English.  
 PS This sequence encodes a Borrelia burgdorferi (Bb) protein of the  
 CC





```
QY 1272 TTGCAAAAAAATTTACAGAGAGAGAAAGGTAAATAACGGGAAGAAG-----1320
Db 128 GTACAAAAAATTTACAGAGAGAGAAAGAAAGAAATTAATGACGGCGATGATCCTAAT 187
QY 1321 -----AAATGATAAGCTGTC 1337
Db 188 GGCAGTGGAAATAATCCGCCACCAGTATTGCCGGAATAATTCACAAATATGCAATTAGTA 247
QY 1338 TTTTTCAGAGAGAAATCAAAAGAGAGATCAAGAAAGAA-----ATGAGCAAGCTGTT 1388
Db 248 TTAAGCAATAGACCAAGTGTGCTCAACAGAGAAAGAAAGAAAGTACAGAGCTGAGCT 307
QY 1389 AATTAGAGAAAGAAATTCGGAGAGAGATGAAGAGTTGTTAATTTAGAGAGAAAGAA 1448
Db 308 AAAGTTGAAGAAATAAAGAAAAACAGAGATACAGAGAAACATTAAGAGAAAGAA 367
QY 1449 TTAGAAGTTAAAAAGAGAGCTGAAGAGATGAAGATAAAGAGAAATAGAGAAACAAAA 1508
Db 368 ATATAGACGACCAACCAACAGAGATTAGCTTAAGCTTAAGAGAGAGAAACAAAA 427
QY 1509 CAAGAAGTGGAAAAAGCACAGAGAGAGAAACCAACGACAGAGAAAGAAAGAAAGAA 1568
Db 428 GAACAAAAAGAGATCAAGAGAGAGCAACAAAGAAAGAGCTAAAGCAGAGAAAGAAAGAA 487
QY 1569 CAAGACAGCAGAGAGAGAGAAAGCAAGAAAGCAAGAGAGAGAGAGAGAGAGCT 1628
Db 488 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
QY 1629 AAAAAACAAATTTAAAAAATTCGGGATAATAGATAGATAGTTGGAAATTTGATGCT 1688
Db 548 GATAACCAATTTAAACACATTTAGCTTAATAGATAGATAGATCAATGAAATTTGATGTT 607
QY 1689 ATAGAAAGTCAACAGAGTGAACCGAGAGAGATTTATAGATTAATTTAGGGGCTGTA 1748
Db 608 ATAAATGGCAACAGAGCTGTAGGCCCAAGAGCGCTTATAGATAGAAATTTAGGGGCTGTG 667
QY 1749 TATGATTATTTTCCGATGACAAACAAAAAGCTATATATAAACATGCGGAGATTTAGAA 1808
Db 668 TATGATGATTTTACCAATGGCAATATTTATACGGCAACTTGGAGGGGTTAGAGAG 727
QY 1809 GATGAGAGCGAGAGATTTGGGAAATTTATTCAGAGAAATTTAGTGAATCTAGAGATGAG 1868
Db 728 GAATCAGAGAGAGAGATTTAGGAAATTTATTCAGAGAAATTTAGTGAATCTAGGAGCGG 787
QY 1869 TTAAGAACCAATTTAAATAAGATATAAAAAATTTATGCCCATGAAATGAGCTCCT 1928
Db 788 CTAGAGAACTAAATTTAATGAGGCAATTAACCATATCTGTTACGAA---GAGCCTAAG 844
QY 1929 CTAAAGAAATCTAGATGTCACCGAAATTTAAGAGAGATTTAGAAAGAAATTAAGTACGGA 1988
Db 845 TTAAGAGAAAGTGTAAATGTTAGCGAAATTTAAGAGAGATTTAGAAAGAAATTAAGTACAA 904
QY 1989 TTAGAGAGAGTAAAGATATCTTAAGACAAATTTCTAATTTTGAAGAAATTTAAGGATAC 2048
Db 905 TTAGAGAGAGTAAAGATATCTTAAGAGATGTTCTAATTTTGAAGAAATTTAAGGATAC 964
QY 2049 ATCAGTTACAGTCAG 2063
Db 965 ATCAGTGACAGTCAG 979
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## RESULT 13

AA61812  
ID AA61812 standard; DNA; 1039 BP.

XX AC AA61812;

XX AC AA61812;

DT 19-JUL-1999 (first entry)

XX B. burgdorferi antigenic protein coding sequence, t5-14.nt.

DE Antigenic protein; vaccine; Lyme disease; infection; detection; ss.

XX

KW

```
XX OS Borrelia burgdorferi.
XX PN WO9859071-A1.
XX PD 30-DEC-1998.
XX PF 18-JUN-1998; 98WO-US012718.
XX PR 20-JUN-1997; 97US-0050359P.
XX PR 22-JUL-1997; 97US-0053344P.
XX PR 22-JUL-1997; 97US-0053377P.
XX PR 03-SEP-1997; 97US-0057483P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (MEDI-) MEDIMMUNE INC.
XX PI Choi GH, Erwin AL, Hanson MS, Lathigra R;
XX WPI; 1999-189980/16.
XX DR P-FSDB; AAY20115.
XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop
XX PT products for the diagnosis, prevention and treatment of diseases caused
XX PT by Borrelia, particularly Lyme disease.
XX PS Claim 1; Page 202; 275pp; English.
XX CC This sequence encodes a Borrelia burgdorferi (Bb) protein of the
XX CC invention, which is suitable for use in a vaccine. The Bb polypeptides
XX CC can be used in vaccines for eliciting protective antibodies to members of
XX CC the Borrelia genus, particularly for the use against Lyme disease in
XX CC humans and animals. They can be used for preventing or attenuating an
XX CC infection caused by a member of the Borrelia genus. The products can also
XX CC be used for detection of members of the Borrelia genus
XX SQ Sequence 1039 BP; 526 A; 94 C; 212 G; 207 T; 0 U; 0 Other;
```

Query Match 15.5%; Score 385.4; DB 2; Length 1039;

Best Local Similarity 63.5%; Pred. No. 5.9e-43;

Matches 606; Conservative 0; Mismatches 346; Indels 3; Gaps 1;

QY 1113 GCACACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGAT 1172

Db 86 GCAAAAGATAAATTTACTTCAAGTAGTTCAAAAGTAGATGAATTAGCAAAAAAATTACAA 145

QY 1173 GCAGACAAATATATAAGGGAAGTTCAAGGATTTTGAAGAGATTTTAGATCCAGTA 1232

Db 146 GAAGAAGATGAAGATAATGAATTAATCGGGCGATGATCCTAATACAGAGCAATAGCA 205

QY 1233 AAGGATAAAAATTTGCTTCAAAATGGTCCAAATAGCAGATGAATTTGCAAAAAAATTACAGAA 1292

Db 206 CTGTTACCAGTATTGCCGGAATATAGTCATGACATCCACCAGTACCAAAAGTAAAGCA 265

QY 1293 GAAGAAAGGTAATAACGGGGAAGAGAAATGATAAGCTGCTTTTACGAGAGAA 1352

Db 266 GCACACAAAGTGGTGTCTCAACAGAGAGACCAAAAGCAAAAGCAAAAGTCTAAGAGATAAGTT 325

QY 1353 TCAAAAGAGGATGAAGAGAAATTTAGCAAGCTGTTAAATTTAGAGAAAAAATGCGGAA 1412

Db 326 GAGGAAGAAAGAGAGTTGTAGAGGAGAAAGAGAGAGAGATAGTAAAGAGAAAA 385

QY 1413 GAGGATGAAGAGATTTGTTAATTTTGAAGAGAGAAATTTAGAGTTAAAGAGACTGAA 1472

Db 386 GTGAGAGAGCAAGCTCAAAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 445

QY 1473 GAACATGAAGATGAAGAGAAATTTAGAGAAACAAAAACAAAGTGGAAAAAGCAGCAAGAA 1532

Db 446 AAACAGAGAGAGCAAAAGCTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 505

QY 1533 AGAAAAACACGACAG 1592

Db 506 GAACAAAAAG 565



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QY 2013 AAAGACAATTCTAAATTTGAAGAAATTAAGGATACATCAGTTACAGTCAGTAAT 2067
DB 1066 GAAAATGAAGATAATTTTGAAGAAATTAAGGATACATTCAGGATAGTAATTCAT 1120

RESULT 15
ID AAX20260/c
XX AAX20260 standard; DNA; 9542 BP.
AC AAX20260;
XX
DT 04-MAY-1999 (first entry)
XX
DE Borrelia burgdorferi polynucleotide sequence #13.
XX
KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW infection; diagnosis; characterisation; detection; ds.
XX
OS Borrelia burgdorferi.
XX
XX WO9858943-A1.
XX
XX 30-DEC-1998.
XX
XX 18-JUN-1998; 98WO-US012764.
XX
XX 20-JUN-1997; 97US-0050359P.
XX
XX 22-JUL-1997; 97US-0053344P.
XX
XX 22-JUL-1997; 97US-0053377P.
XX
XX 03-SEP-1997; 97US-0057483P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;
XX Smith HO;
XX WPI; 1999-081217/07.
XX
XX New isolated Borrelia burgdorferi nucleic acids - used to develop
XX products for the detection, diagnosis, characterisation, prevention and
XX therapy of infections, particularly Lyme disease.
XX
XX Claim 1; Page 920-925; 1128pp; English.
XX
XX AAX20248 to AAX20402 represent polynucleotide sequences isolated from
XX Borrelia burgdorferi (Bb). Products derived from Bb can be used for the
XX detection, diagnosis, characterisation, prevention and therapy of Bb
XX infections, e.g. Lyme disease. They can also be used for the production
XX of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of
XX mobile, spiral-shaped bacteria called Spirochetes. Spirochetes are
XX pathogenic in humans and Borrelia causes epidemic and endemic relapsing
XX fever, and Lyme borreliosis, more commonly known as Lyme disease
XX
XX Sequence 9542 BP; 3812 A; 1160 C; 1113 G; 3457 T; 0 U; 0 Other;
XX
XX Query Match 13.5%; Score 336.8; DB 2; Length 9542;
XX Best Local Similarity 68.6%; Pred. No. 1.6e-36;
XX Matches 520; Conservative 0; Mismatches 212; Indels 26; Gaps 3;
XX
QY 1 ATTTATTACAGAACCCCTGACCTTTTGAGAGATTTTGAATTTATTAGAAATATGGA 60
DB 4722 ATTTACGCTTCAAAACCCCACTTTCTAAGTAACCTTTTGAATTTTATTAGCAATCAGT 4663
QY 61 TAATGCTAATTTGGTTGCTTTAAACTATGTTTGGATTTTGAAGAAATTAAGTACGTC 120
DB 4662 CAAATGCTAATTCGATATATCTTTAAACCTATGTTTGGTTTGAAGAAATTAAGTACGTC 4603
QY 121 TTGTATCAAGATTTTCTCATTAATGATTTTGTGCTGCTGTTGATAGCTCGAAT 180
DB 4602 TAGTATTAAAGATTTTCTTTTGAAGTAAATTCGTGCTACTTTTGAATAGCAATTAAT 4543
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QY 181 CTTCGAGTTGATAACAAATTTCTCTAATACAAGTTACATTTCTTTTGGCCACATTTA 240
DB 4542 CTTTTCGGTTATAACAAATTCCTCTAGTACAAGTAGTAAATTTTCTTTTGGCCACATTTA 4483
QY 241 CTTTATATGTTGATAAAAGTTTTCCTATTTTGGCTTTAAAAAGTTGAAATATCTTGCATTT 300
DB 4482 CTTTATATGTTGATAAAAGTTTTCCTATTTTGGCTTTAAAAAGTTGAAATATCTTGCATTT 4423
QY 301 TTACTTTTTCAGTTTCGGTCCCTCGAGCCACTTATTCGAGTAATGTAAACCAAC 360
DB 4422 TTACTTTTTCAGTTTCGGTCCCTCGAGCCACTTATTCGAGTAGGTGACAAACATC 4363
QY 361 CAGATATTGGATCAGCTTGTAAAGAGTTTGTATGCAATTTTCAATTTAGTTTGCCTAATTT 420
DB 4362 CAGCTATTGGTCAATTTGTTTAAATGCTTTGACACATTTTATAATTAATTTGATTAGTTT 4303
QY 421 TTGGGTCAAATAAAATTTAGGAGTTGGCTTTGAAGCTTT-----TTTAGTAG 468
DB 4302 TTGGATTTAAGTACACACTTAGCAGTGGTTTGAATTTTCTGTTTATTTCTTTTAT 4243
QY 469 GCTTAGAGAAATTTTGTAGTAAATTTTAAAGAAATTTTGTATTTTCAATTTATTAG----- 520
DB 4242 TTTTCGGTTAATTTTATTTTATTTTAAAGTTTATTTTATCTATTTATTAGTAGTA 4183
QY 521 -TTTTGATGATCTTGTAAATTAAGCATAAATCTATGTTGAAATTTTAAATTA 579
DB 4182 TTTTTCGATTATCTCGTGAATTTTAAAGCAATCTCTCTGCGGTGATTTTGTAAATCTA 4123
QY 580 GATTAATTTATTCATGTCCTAATAAT-----CCCTCCCTTATAAGTGTACTTTTAAATTA 634
DB 4122 AAAAATTTATCAATTTCCATTAATTAATCTCCACTTTTAAATCAACAAATTAATATCAA 4063
QY 635 GTAAAAGTAAATAAAATTTGATTAATAATTTATTTTACCAAAAAACAAAAAAT 694
DB 4062 AATAAATAATTAATTAATTTATTTATTTCTATGTCATAGTTTCTATGATATCAAAAAAT 4003
QY 695 TAGTCAATTTGTGGCTTCTCATTTGCATGCAAAATTT 732
DB 4002 CACTAAAAATTTTGAGATTTTGTGTTATTAAATTT 3965
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Search completed: July 29, 2004, 16:32:51  
Job time : 993 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: July 29, 2004, 15:00:53 ; Search time 9526 Seconds  
(without alignments)  
11315.781 Million cell updates/sec  
Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTATACAGAACCCCT.....TTAAGACACTTIGAAAGA 2487

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2485	99.9	52971	1	AE001584	AE001584 Borrelia
2	1424.4	57.3	1426	1	AF020657	AF020657 Borrelia
3	1149.6	46.2	5108	1	BU44914	U44914 Borrelia bu
4	1088	43.7	3468	1	AF077603	AF077603 Borrelia
5	1045	42.0	5579	1	BU42599	U42599 Borrelia bu
6	990	38.8	3662	1	BU18292	U18292 Borrelia bu
7	970	38.0	3085	1	AE001580	AE001580 Borrelia
8	966.8	38.9	30750	1	AE001575	AE001575 Borrelia
9	963.8	38.8	8942	1	AF023853	AF023853 Borrelia
10	947.6	38.1	30651	1	AE001581	AE001581 Borrelia
11	906	36.4	30800	1	AE001579	AE001579 Borrelia
12	900.6	36.2	3231	1	BU30617	U30617 Borrelia bu
13	875.6	35.2	4283	1	BU44912	U44912 Borrelia bu
14	874.2	35.2	29838	1	AE001578	AE001578 Borrelia
15	873	35.1	3904	1	BU42598	U42598 Borrelia bu
16	873	35.1	30223	1	AE001576	AE001576 Borrelia
17	866.6	34.8	7064	1	BU19754	U19754 Borrelia bu
18	863.8	34.7	21170	1	AF169008	AF169008 Borrelia
19	861.6	34.6	3209	1	AF023852	AF023852 Borrelia
20	783.8	31.5	30299	1	AE001577	AE001577 Borrelia
21	772.8	31.1	2849	1	BU44913	U44913 Borrelia bu
22	721.4	29.0	2119	1	AF077602	AF077602 Borrelia
23	699.4	28.1	2034	1	AF005056	AF005056 Borrelia
24	504	20.3	2196	1	BU78764	U78764 Borrelia bu
25	494.6	19.9	2261	1	BU72996	U72996 Borrelia bu
26	438	17.6	1950	1	AY142081	AY142081 Borrelia
27	414.2	16.7	1290	1	AY142087	AY142087 Borrelia
28	400.8	16.1	2010	1	AY142086	AY142086 Borrelia
29	389.8	15.7	2041	1	BU72998	U72998 Borrelia bu
30	380.8	15.3	8303	1	BU03641	U03641 Borrelia bu
31	367.8	14.8	1665	1	AY142084	AY142084 Borrelia
32	336.8	13.5	8720	1	AF292711	AF292711 Borrelia
33	336.8	13.5	9386	1	AE000791	AE000791 Borrelia
34	336.2	13.5	1693	1	AY142077	AY142077 Borrelia
35	311.6	12.5	585	1	AF011453	AF011453 Borrelia
36	297.6	12.0	1199	1	BU72997	U72997 Borrelia bu
37	294.6	11.8	1860	1	AY142082	AY142082 Borrelia
38	258.2	10.4	1199	1	AY142078	AY142078 Borrelia
39	248.2	10.0	44010	1	AB073701	AB073701 Borrelia
40	237.8	9.6	1524	1	BBOSPG	X82409 B.burgdorfe
41	234	9.4	1453	8	AJ591978	AJ591978 Arabidops
42	231.6	9.3	10099	1	AF123078	AF123078 Borrelia
43	230.8	9.3	1434	8	AJ592058	AJ592058 Arabidops
44	229.4	9.2	1260	1	AY142080	AY142080 Borrelia
45	223	9.0	1407	8	AJ592026	AJ592026 Arabidops

ALIGNMENTS

RESULT 1  
AE001584  
LOCUS AE001584 52971 bp DNA linear BCT 17-MAR-2003  
DEFINITION Borrelia burgdorferi B31 plasmid lp56, complete plasmid sequence.  
ACCESSION AE001584  
VERSION AE001584.1 GI:6382393  
KEYWORDS  
SOURCE Borrelia burgdorferi B31  
ORGANISM Borrelia burgdorferi B31  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
1 (bases 1 to 52971)  
REFERENCE  
AUTHORS  
CsaJens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B.,  
Ros,J., Iathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Hatt,D.,  
Hickey,E., Gwinn,M., White,O. and Fraser,C.M.

TITLE A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi

JOURNAL Mol. Microbiol. 35 (3), 490-516 (2000)

MEDLINE 20138354

PUBMED 10672174

REFERENCE 2 (bases 1 to 52971)

AUTHORS Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van Vugt R., Palmer N., Haft D., Rosa P. and Stevenson B.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

FEATURES

source 1..52971

organism="Borrelia burgdorferi B31"

mol\_type="genomic DNA"

db\_xref="taxon:224326"

plasmid="lp56"

279..548

/gene="BBQ01"

279..548

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/note="similar to GB:U03641 PID:458212 percent identity: 67.53; identified by sequence similarity; putative"

/codon\_start=1

/transl\_table=11

/product="conserved hypothetical protein"

/protein\_id="AA07704.1"

db\_xref="GI:6382394"

/translation="MTKYLAILVARPKDAEICISGVNKKOTENYKLVLLCLLF GYLGVHRFYVIGTGLLYLFTGFYVGLDLIRITNKFCN"

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/note="hypothetical protein; identified by Glimmer2; putative"

/codon\_start=1

/transl\_table=11

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db\_xref="GI:6382428"

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856..1407

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856..1407

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/translation="MRILVGVFIIALALIGCYLPDQCAVOTFFENSEIDMGSDIEVTEGIFSSKLYASSHRLVLEIKTLISLKDNYDVPVVDYNEEYFNKFDLIGS EQSKDLIKLGRVNEONNFKSEVWLVISLSELISPDIKYSGEBSPEYDFRFRP TAYQYKVREREINRTINGKIL"

1404..2268

/gene="BBQ04"

/note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:520778 percent identity: 93.50; identified by sequence similarity; putative; protein p23, authentic frameshift"

2744..3496

/gene="BBQ05"

2744..3496

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/note="similar to GP:1553115 percent identity: 53.30; identified by sequence similarity; putative"

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/product="antigen, P35, putative"

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db\_xref="GI:6382396"

/translation="MKYVICVVFLLNACNSDFSTNOBDIKVPSEKSKSMEASS KEDPNKKIKNLILNLIETANHEKKEKEMOEPSDOYGILAFQELDLVSGKI SEDTPQSKFRKNTYPLSAIDNWKDLSEIRNSGOIQLFNINRFGGIFDGLN HVYSKDIILGGLEILDKLKSEFKLSIKETFSKLNQLLLDYKNDKHRTETNK LKSHTTALPEQLDKEDAEYEPKNQIFSINL"

3623..4108

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db\_xref="GI:6382397"

/translation="MGIFAQEKLKGVGDIATVMKYESKATILAPLLNIFLSLIG SFVQGYIGGALLGSQVGLGILIMAGYMGIDGIFVETATVITGVSIGGLLIA ASYITGIIIPFKFANRYNADLKKRLGIALAGLEPNFDIGINGDSNRLKNPIEQYTW G"

complement(4249..4986)

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complement(4249..4986)

/gene="BBQ07"

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complement(5069..5830)

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complement(5069..5830)

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db\_xref="GI:6382399"

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complement(5803..6339)

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complement(6336..6674)

gene

CDS

gene

CDS

gene

CDS

gene

CDS

gene

CDS

gene

CDS

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QY	481 TTTTGTAGTGAATTTTAAAGATTTTGTTCATTTATTAGTTTGTAGTGAATTTTGTGAATA 540	
Db	29389 TTTTGTAGTGAATTTTAAAGATTTTGTTCATTTATTAGTTTGTAGTGAATTTTGTGAATA 29448	
QY	541 ATTTAAGCATAAAACTCTATGTTGAATTTTAAATTAAGATAAATTTATTCATGTCCTAA 600	
Db	29449 ATTTAAGCATAAAACTCTATGTTGAATTTTAAATTAAGATAAATTTATTCATGTCCTAA 29508	
QY	601 AATCCCTCCTTATTAAGTGTCTATTTTAAATTAAGTAAAGTAATAAAATTTGATTAATA 660	
Db	29509 AATCCCTCCTTATTAAGTGTCTATTTTAAATTAAGTAAAGTAATAAAATTTGATTAATA 29568	
QY	661 ATGTAAATTTATATTTTACCAAAAACAAAATAATTTAGTCAAAATTTGTGGCTTCTCAT 720	
Db	29569 ATGTAAATTTATATTTTACCAAAAACAAAATAATTTAGTCAAAATTTGTGGCTTCTCAT 29628	
QY	721 CATGCAAAAATTTGGATTGTAGGATAGCTGTGATATAACACAGAGAGGCAATTTTAAAGGG 780	
Db	29629 CATGCAAAAATTTGGATTGTAGGATAGCTGTGATATAACACAGAGAGGCAATTTTAAAGGG 29688	
QY	781 GCACCTAAGAAGATACCTATCTTAACTGATATATAGCAAGACTTTGAAATTTAAGTT 840	
Db	29689 GCACCTAAGAAGATACCTATCTTAACTGATATATAGCAAGACTTTGAAATTTAAGTT 29748	
QY	841 GTATGTGTTTTGTAGTCTTTTATATAGCAGGAGGCAATTTGCAATGGAGAGATTTTAGGGA 900	
Db	29749 GTATGTGTTTTGTAGTCTTTTATATAGCAGGAGGCAATTTGCAATGGAGAGATTTTAGGGA 29808	
QY	901 GTTGATTAATAATTTATTTGGCTTTTGTATATATGTAATAGCTGAATGAACAAAATTTAT 960	
Db	29809 GTTGATTAATAATTTATTTGGCTTTTGTATATATGTAATAGCTGAATGAACAAAATTTAT 29868	
QY	961 ATATTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTGTAAGCTTTAGGCTTATGG 1020	
Db	29869 ATATTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTGTAAGCTTTAGGCTTATGG 29928	
QY	1021 AGTGATTATCAATAAAAAATTTGAAATTTATTTATTTGTGCTGTAATTTGTGCTGATA 1080	
Db	29929 AGTGATTATCAATAAAAAATTTGAAATTTATTTATTTGTGCTGTAATTTGTGCTGATA 29988	
QY	1081 GTTCTTGCAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAG 1140	
Db	29989 GTTCTTGCAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAG 30048	
QY	1141 ATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAG 1200	
Db	30049 ATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAG 30108	
QY	1201 AAGGATTTTGAAGAAAGATTTTAGATCCAGTAAAGGATAAAATTTGCTTCAATGGTCAA 1260	
Db	30109 AAGGATTTTGAAGAAAGATTTTAGATCCAGTAAAGGATAAAATTTGCTTCAATGGTCAA 30168	
QY	1261 TAGCAGATGAATTTGGCAAAAAATTTACAAGAGAGAGGATAAAATTAACGGGGAAGAG 1320	
Db	30169 TAGCAGATGAATTTGGCAAAAAATTTACAAGAGAGAGGATAAAATTAACGGGGAAGAG 30228	
QY	1321 AAAATGATAAGCTGTCTTTTAGGAGAGAAATCAAAAGAGGATGAAGAGAAATAGAGC 1380	
Db	30229 AAAATGATAAGCTGTCTTTTAGGAGAGAAATCAAAAGAGGATGAAGAGAAATAGAGC 30288	
QY	1381 AAGCTGTTTATTTAGAGAGAAATTAATCGGAGAGGATAGAAAGTTGTTAATTTAGAG 1440	
Db	30289 AAGCTGTTTATTTAGAGAGAAATTAATCGGAGAGGATAGAAAGTTGTTAATTTAGAG 30348	
QY	1441 AGAAAGAAATTAGAAGTTTAAAGAGAGAGCTGAAGAGATGAAGATAAGAGAGAAATAGAG 1500	
Db	30349 AGAAAGAAATTAGAAGTTTAAAGAGAGAGCTGAAGAGATGAAGATAAGAGAGAAATAGAG 30408	

Query Match		99.9%; Score 2485; DB 1; Length 52971;
Best Local Similarity		99.9%; Pred. No. 2.6e-263;
Matches 2485; Conservative		0; Mismatches 2; Indels 0; Gaps 0;
QY	1	ATTTATTACAGAAACCCCTGACTTTTGTGAGAGATTTTGTGAATTTATTAGAAATATGGA 60
Db	28909	ATTTATTACAGAAACCCCTGACTTTTGTGAGAGATTTTGTGAATTTATTAGAAATATGGA 28968
QY	61	TAATGCTAATTTGGTTGCTTTAAACTATGTTTGGATTTTGAAGAAATTAAGTACGTC 120
Db	28969	TAATGCTAATTTGGTTGCTTTAAACTATGTTTGGATTTTGAAGAAATTAAGTACGTC 29028
QY	121	TTGATCAAGATTTTCTCAATTAAGATTTTGTGCTGTTTGGATAGGCTCGAAT 180
Db	29029	TTGATCAAGATTTTCTCAATTAAGATTTTGTGCTGTTTGGATAGGCTCGAAT 29088
QY	181	CTTCTGAGTTGATAACAATTTCTCTAATACAGTTACATTTCTTTTGTGCTGCTTCAATTTA 240
Db	29089	CTTCTGAGTTGATAACAATTTCTCTAATACAGTTACATTTCTTTTGTGCTGCTTCAATTTA 29148
QY	241	CTTTTATGTTGATAAAGTTTTCATTTTGGTAAAGAGTTGAAATATCTTGCAATTT 300
Db	29149	CTTTTATGTTGATAAAGTTTTCATTTTGGTAAAGAGTTGAAATATCTTGCAATTT 29208
QY	301	TTACTTTTTCGAGTTTCGGTGGCCCTGCAGCCACTTATTCGAGTAAATGTAAGAAACCAAC 360
Db	29209	TTACTTTTTCGAGTTTCGGTGGCCCTGCAGCCACTTATTCGAGTAAATGTAAGAAACCAAC 29268
QY	361	CAGATATTGATCAGCTTGTTTAAGAGTTTGTGATGCAATTTTCAATTTAGTTTGCCTAATTT 420
Db	29269	CAGATATTGATCAGCTTGTTTAAGAGTTTGTGATGCAATTTTCAATTTAGTTTGCCTAATTT 29328







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CDS	/gene="erpC" 1736..2275 /gene="erpC" /codon_start=1 /transl_table=11 /product="ErpC" /protein_id="AAC34910.1" /db_xref="GI:1373143" /translation="MNKMKWFIICFIALISSCKNHTLYDQSGNGEAKVKIKLFSEF TVIKNNNSNNWADIGLVVRKEEDGIEIETGLAVGKSDSTPAGYATATPFLSESVN NFIAKNTEGGSPXTSLVYKDEQSNANGIQNKETITKIEKIDDFEVIIFLGLDKIDS GDKVVEYAILLEDLKNLK"
gene	2303..3319
CDS	/gene="erpD" 2303..3319 /gene="erpD" /codon_start=1 /transl_table=11 /product="ErpD" /protein_id="AAC34911.1" /db_xref="GI:1373144" /translation="MNQKAFIIICAVFAIISCKNYATSKDILKQNPEKIKGFLDPTKD KITSIQPKVDEVAUKQBERELMQDDPSGINPPPTLLENGNTNLVIPAKSAEQ SGQBEKSKREERKKQBEKKVEQONKQEKERNVEKQKQBEERQKQOE EARAKAKEKREERKKQBEKKVKGRIKLTLDKINEIRDIKGOTSIGABEV DKTGPIDDPDTSSSIPFTMGDLVEEDLELRLLKELSSEARDSLSRLKLVNDOPY IIDRSTEPOLKONVSVEISKSDLDELKSKLEVEKYLEDKDNFEIKYKVAGSEDNY DEED"
ORIGIN	
Query Match	46.2%; Score 1149.6; DB 1; Length 5108;
Best Local Similarity	67.6%; Pred. No. 3.9e-117;
Matches 2043; Conservative	0; Mismatches 441; Indels 540; Gaps 9;
Qy	1 ATTATTATCACGAAACCCCTGACTTTTGTGAGAAGATTTTTGAATTTATTAGAATAATGGA 60
Dd	708 ATTTATTACAGAAACCCCGAATTTTAAAGAAGATTTTTAAATTTATTAGAATAATGGA 767
Qy	61 TAATGCTAAATTTGGTGTCCTTTAAACCTATGTTTGGATTTTGCAGAAAAATAAGTAGCTC 120
Dd	768 TAATGCTAAATTTGGTGTCCTTTAAACTATATGTTTGGATTTTGGAAAAATAAGTAGCTC 827
Qy	121 TTGTATCAAGATTTTCTCATTAATAATGATTTTGTGCTGTTTGGATAGCCTCGAACT 180
Dd	828 TTGTATCAAGATTTTCTCATTAATAATGATTTTGTGCTGTTTGGATAGCCTCGAACT 887
Qy	181 CTCTGAGTTGATACAATTTCTCTATACAAGTTACATTTCTTTTTTTTGGCACATTTA 240
Dd	888 CTTCTGAGTTGATACAATTTCTCTAATACAAGTTACATTTCTTTTTTTTGGCACATTTA 947
Qy	241 CTTTATTGTTGTATAAAGTTTTTCCATTTTGTCTTAAAAAAGTTGAAATATCTTGCATTT 300
Dd	948 CTTTATTGTTGTATAAAGTTTTTCCATTTTGTCTTAAAAAAGTTGAAATATCTTGCATTT 1007
Qy	301 TTACTTTTTGCAAGTTGCGTGCCCTGCAGGCCACTTATTGCGAGTAAATGTAAAACCAC 360
Dd	1008 TTACTTTTTGCAAGTTGCGTGCCCTGCAGGCCACTTATTGCGAGTAAATGTAAAACCAC 1067
Qy	361 CAGATATTGATCAGCTTGTTTAAAGAGTTTGTATGCAATTTTCAATFAGTTTGCCTAATTT 420
Dd	1068 CAGATATTGATCAGCTTGTTTAAAGAGTTTGTATGCAATTTTCAATFAGTTTGCCTAATTT 1127
Qy	421 TTGGGGTCAAATAAAATTTAGGAGTTGGCTTTGAGCGCTTTTATAGTAGGCTTATAGAGAAA 480
Dd	1128 TTGGGGTCAAATAAAATTTAGGAGTTGGCTTTGAGCGCTTTTATAGTAGGCTTATAGAGAAA 1187
Qy	481 TTTTATTGATGATTTTAAAGAAATTTTGTTTTCAATTTATTAGTTTGTGATGATCTTGTAATA 540
Dd	1188 TTTTATTGATGATTTTAAAGAAATTTTATTTCAATTTATTAGTTTGTGATGATCTTGTAATA 1247
Qy	541 ATTTAAGCATAAATCTATGTTGAAATTTATTTAAATTAAGATAATATTATTCATGTCCTATA 600

QY	1192	GGAAAGTTCAAGGATTTT	TAGAAAAGATTTT	TAGATCCAGTAAAGGATAAAAA	TGCTTCAA	1251
DB	2398	AAAATCCGAAGGGGAAAT	TAAAGGATTTT	TAGATCCAAACAAAGGATAAAAT	TACTTCCAA	2447
QY	1252	ATGTCCTAATAGCAGATGAA	TTGGCAAAAAAATT	---ACAGAAAGAAAGAAAAGGTAATA	1308	
DB	2448	TTGGCCCAAAAGTAGTAGTGA	CTACGAAAAAATTT	GAAACCAAGAAAGAGAAATTAATGC	2507	
QY	1309	ACGGGGAAGAGAAAANTGAT	ATAAAGCTGTCTTTT	TAGAGAGAGATCAAAGAGAGTGAAG	1368	
DB	2508	AGGCGGATGATCTTAATGG	CAGCGGAATAAATTCG	CCACCACCAATTACTTGA	2567	
QY	1369	AAGAAAATGACCAAGCTGT	TAAATTTAGAGAAAAAAT	TGCGACAGGATAAGAAAGCTTG	1428	
DB	2568	ACGACAATACACTAGTACCA	ATAGCAAAATCAGCAGAAC	AACAGTGGTGATCNAAGAAG	2627	
QY	1429	TTAATTTAG---	---AAGAGAAAGAAAT	TAGAAGTAAAAAGAGACTGAAGAGATGAAGATA	1485	
DB	2628	AAAATCAGGAAAAGTTGAG	AAAAAAGAAAACCAAGAG	AGTAAAGAAAGAAAAAGCTAG	2687	
QY	1486	AAGAAAGAAA-----	---TAGAGAAA	CAAAAAACAAGAAGTGGAAAGACCAAGAAAGAAAC	1539	
DB	2688	AGGAACAAACCAAGAAAAA	AGCAAAAAGAGAGAGAA	ACGTTAAGAGAGAAAAC	2747	
QY	1540	AACGACAGAGAAAAAGAA	ACGAAAAAACH-----	-----AGAACGC	1578	
DB	2748	AAAAACAGAGAGAAAGAA	AGCAAAAAACACAGGAA	GAAGCTAGGGCTTAAAGCAGAAAAAG	2807	
QY	1579	AAGAAAGAAAAGAAACG	AAACGACAGAA	CAAAAGAAAAGAGAGAGCTAAAAAA	1638	
DB	2808	AAAACGAGAAAGAGAGAA	AAAAACAAAACAGAGAA	AGAAAGAAAGAAAGTTAAGGCGAGAA	2867	
QY	1639	TTAAAAAATTGCGGATTA	AAATAGATGAGATAGT	TGGAATATTGATGGTATAGAAAGTC	1698	
DB	2868	TTAAAAACACTTACAGAT	AAAAATAAATGAGATA	AAACAGAGATATTGATGGTATAAAAAGTC	2927	
QY	1699	AAACAAGTGTAAAAACCG	AAAGCAGTTATAGATA	AAAAATTCAGGGCCCTGTATGATTATT	1758	
DB	2928	AACTACATAGAGAGAGAG	AGAGAGTTAGAGATAA	AAATTCAGAACCCATATTATGATGATT	2987	
QY	1759	TTACCGATGACAA	CAAAAAAGCTATATATA	AAAAACATGGGAGATTTAGAAAGATGAAGAAG	1818	
DB	2988	TTAC--TGATAGTAGTAG	CTCTATACGTACA	CTTGGGAGATCTGGAATATGAAGAAG	3044	
QY	1819	CGCAAGGATTGGGAAAT	TATTGGAAGAAATGAGT	GTGATATAGAGATGAGCTTAAAGACCA	1878	
DB	3045	ATTTAGAATTAGGAAGCT	ATTAAAGAAATGAGT	GAACTAGACAGGCTTTAAGAACCTA	3104	
QY	1879	AAITAAATAAGATATA	AAAAAATA-----	TTATGCCCATGAAATGAGCCCTCTCTAA	1932	
DB	3105	AAITAAATGTAGACA	ATCAACCATATATTAT	TGATACTAGAAGCAGCTGAACCCCAATTAA	3164	
QY	1933	ARGAAATGTAGATGT	CAGCGAAATTAAGAGAG	NTTTAGAAAAAGTAAATCAGGATTAG	1992	
DB	3165	AGATAATGTAAAGTGT	GTAGCGAAATTAATTCAG	ACTTAGATGAACCTAAAAATCAAAATTTAG	3224	
QY	1993	AAAAGGTTAAAGAAAT	ATCTTTAAAGACAAAT	TCTAAATTTGAAGAAATTAAGGATACATCA	2052	
DB	3225	AAGAAGTTAAAGAAAT	CTTTGAAGATAAAGATA	TAATTTTGAAGAAATTAAGATACGTTG	3284	
QY	2053	GTTCACAGTCAG-----	-----TAATTTAT	TTCGATGCTTTTAGATGTAACTAAATTTACGT	2104	
DB	3285	CTGGTAGTAGGATA	TAATTTAGTGAAGAGAT	TAAATTTTATAGATATACTAAATTTTGTAT	3344	
QY	2105	ACAAAAATAACAGCTAG	TAGAAAAGTTCACTGGC	TGTATTTTTTTTGTAGATTTTCATTG	2164	
DB	3345	ACAAAAATAACAGCTAG	TTGCAAGAATTCGTAG	TGTTATTTTTTTTGTAGATTTTCATTG	3404	
QY	2165	TTATGAATATAGAAA	TGTTTTCTTATCAAA	CTTTTCAATTTAAAAAGTG-CAAAAACCTATTG	2223	
DB	3405	TTATGAATATAGAAA	TGTTTTCTTATCAAA	AGTTTCTATTCAAAAGTGCCAAAACCTATTG	3464	

QY	2224	CTAAATATGTTGTTTATTTATATCTCTCTAGAGCTATGACGTATACAATGAGATTTC	2283
DB	3465	TTAAATATATTTGTTTATTTATATCTCTCTAGAGTTTATGATGAATATAAATGATATTTC	3524
QY	2284	GATTTTGAATGATAATTTATATAAGAAAAACAAAAAGAAAAATAGATAAACTTATAAACCAAG	2343
DB	3525	GATTTTATGATATATTTATATAAGAAACAAAAAGAAAAATAGATAAACTTATAAACCAAG	3584
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DB	3585	CTCTATTTAACTAGCCAAATAACTCTTAAGCAAAAAAGAAAAAGAAAAATNTACAGTGTGTTGAA	3644
QY	2404	AGAATGCAAAAAATACGTAAATAAAAAACCGGAAAAAGTGTCTTTTAGTAATCGGAAAAAGAA	2463
DB	3645	AAATGCAAAAGTACGTATATAAACCGGAAAAAGTGTCTTTTAGTAATCGGAAAAAGAA	3704
QY	2464	TTTCTTAAGACACTTTTGAAAGA	2487
DB	3705	TTTCTTAAGACACTTTTGAAAGA	3728
RESULT 4			
LOCUS	AF077603	3468 bp DNA linear BCT 29-APR-1999	
DEFINITION	Borrelia burgdorferi strain 297 plasmid-encoded ElpA2 protein (elpA2) gene, complete cds; and unknown genes.		
ACCESSION	AF077603		
VERSION	AF077603.1	GI:4704437	
KEYWORDS			
SOURCE	Borrelia burgdorferi (Lyme disease spirochete)		
ORGANISM	Borrelia burgdorferi		
REFERENCE	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;		
AUTHORS	Borrelia burgdorferi group.		
TITLE	1 (bases 1 to 3468)		
	Akins,D.R., Calmano,M.J., Yang,X., Cerna,F., Norgard,M.V. and		
	Radolf,J.D.		
	Molecular and evolutionary analysis of Borrelia burgdorferi 297		
	circular plasmid-encoded lipoproteins with OspE- and OspF-like		
	leader peptides		
	Infect. Immun. 67 (3), 1526-1532 (1999)		
JOURNAL			
MEDLINE	99150296		
PMED	10024506		
AUTHORS	2 (bases 1 to 3468)		
	Akins,D.R., Calmano,M.J., Yang,X., Hagman,K.E., Cerna,F.,		
	Norgard,M.V. and Radolf,J.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JUL-1998) Internal Medicine, UT Southwestern Med.		
FEATURES	School, 5323 Harry Hines Blvd., Dallas, TX 75235, USA		
source	Location/Qualifiers		
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## ORIGIN

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Best Local Similarity 70.1%; Pred. No. 2.4e-110;
Matches 1620; Conservative 0; Mismatches 645; Indels 45; Gaps 10;

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DB 328 CTTCAGAGTTGATAACAATTTCTATAACAAGTTACATTTCTTTTGTGCTGTTTGGATAGCCTCGAAT 387
QY 240 ACTTTATGTTGATAAAGTTTTCATTTTTCGTTTAAAGAGTTGAAATATCTTCATTT 299
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Qy 61 TAATGCTAAATTTGGTGTCTTTAAACTATATGTTTGGATTTTGAAGAAATTAAGTACGTC 120
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Qy 4490 TAATGCTAAATTTGGTGTCTTTAAACTATATGTTTGGATTTTGAAGAAATTAAGTACGTC 4549
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Db |||
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Qy 4610 CTTCTGAGTTGATAACAAATTTCTTAACAAGTACATTTCTTTTGGTCCACATTTA 4669
Db |||
Qy 241 CTTTATGTTGATAAAGTTTTCATTTTGCCTTAAAGTTGAATATCTTGATTT 300
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Db |||
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Db |||
Qy 4730 TTACTTTTTCAGTTCGGTCCCTCGCAGCCTTATTTGGAGTAAATGTAAGAACCAAC 4789
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Db |||
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Qy 5090 ATGTAATTTATTTTACCAAAACCAAAATTTAGTCAATTTGTGCTGCTCTCATTTG 5149
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Qy 721 CATCAAAATTTGATTTGATGATGCTGTGATAAATCAGAAAGGCAATTTTAAAGGGT 780
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Db 5570 A 5570

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ACCESSION U18292
VERSION U18292.1 GI:3309519
KEYWORDS
SOURCE Borrelia burgdorferi (Lyme disease spirochete)
ORGANISM Borrelia burgdorferi
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
Borrelia burgdorferi group.
REFERENCE 1 (bases 1 to 3662)
AUTHORS Akina,D.R., Porcella,S.F., Popova,T.G., Shevchenko,D., Baker,S.I.,
Li,M., Norgard,M.V. and Radolf,J.D.
TITLE Evidence for in vivo but not in vitro expression of a Borrelia
burgdorferi outer surface protein F (OspF) homologue
JOURNAL Mol. Microbiol. 18 (3), 507-520 (1995)
MEDLINE 96342380
PUBMED 8748034
REFERENCE 2 (bases 1 to 3662)
AUTHORS Akina,D.R.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-1994) Darrin R. Akina, Molecular Microbiology, UT
Southwestern Med. School at Dallas, 5323 Harry Hines Blvd., Dallas,
TX 75235-9048, USA
REFERENCE 3 (bases 1 to 3662)
AUTHORS Akina,D.R.
TITLE Direct Submission
JOURNAL Submitted (13-JUL-1998) Darrin R. Akina, Molecular Microbiology, UT
Southwestern Med. School at Dallas, 5323 Harry Hines Blvd., Dallas,
TX 75235-9048, USA
REMARK Sequence update by submitter
COMMENT On Jul 13, 1998 this sequence version replaced gi:1052863.
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ches 1443; Conservative 0; Mismatches 590; Indels 29; Gaps 7;

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121 TTGTATCAAGATTTTCTCATTAATAATGATTTTGTGTGCTGTTTGGATAGCCTCAACT 180
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181 CTTCTGAGTTGATAACAATTTCTCTAATAAGTTACATTTCTTTTTTGGCACATTTA 240
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DEFINITION			
ACCESSION			
VERSION			
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ORGANISM			
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AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			

REFERENCE	2	(bases 1 to 30885)
AUTHORS	Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Lathigra, R., White, O., Dodson, R., Hickey, E.K., Gwinn, M., Peterson, J., van Vugt, R., Palmer, N., Haft, D., Rosa, P. and Stevenson, B.	
TITLE	Direct Submission	
JOURNAL	Submitted (11-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA	
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 VERSION AE001581.1 GI:6382346  
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 Casjens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B.,  
 Rosa,P., Lathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Haft,D.,  
 Hickey,E., Gwinn,M., White,O. and Fraser,C.M.  
 A bacterial genome in flux: the twelve linear and nine circular  
 extrachromosomal DNAs in an infectious isolate of the Lyme disease  
 spirochete Borrelia burgdorferi  
 Mol. Microbiol. 35 (3), 490-516 (2000)  
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 PUBMED 10672174  
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 AUTHORS  
 Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R.,  
 White,O., Dodson,R., Hickey,E.K., Gwinn,M., Peterson,J.,  
 van-Vugt,R., Palmer,N., Haft,D., Rosa,P. and Stevenson,B.  
 Direct Submission  
 Submitted (11-NOV-1999) The Institute for Genomic Research, 9712  
 Medical Center Dr, Rockville, MD 20850, USA  
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 Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R.,  
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 VERSION AE001579.1 GI:6382257  
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 Casjens, S., Palmer, N., van Vugt, R., Huang, W.M., Stevenson, B.,  
 Rosa, P., Lathigra, R., Sutton, G., Peterson, J., Dodson, R.J., Haft, D.,  
 Hickey, E., Gwinn, M., White, O. and Fraser, C.M.  
 A bacterial genome in flux: the twelve linear and nine circular  
 extrachromosomal DNAs in an infectious isolate of the Lyme disease  
 spirochete Borrelia burgdorferi  
 Mol. Microbiol. 35 (3), 490-516 (2000)  
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 REFERENCE 2 (bases 1 to 30800)  
 AUTHORS Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Lathigra, R.,  
 White, O., Dodson, R., Hickey, E.K., Gwinn, M., Peterson, J.,  
 van Vugt, R., Palmer, N., Haft, D., Rosa, P. and Stevenson, B.  
 Direct Submission  
 Submitted (11-NOV-1999) The Institute for Genomic Research, 9712  
 Medical Center Dr, Rockville, MD 20850, USA  
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VERSION U30617.1 GT:3309515  
KEYWORDS  
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ORGANISM Borrelia burgdorferi  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
REFERENCE 1 (bases 1 to 3231)  
AUTHORS Akins,D.R., Porcella,S.F., Popova,T.G., Shevchenko,D., Baker,S.I.,  
Li,M., Norgard,M.V. and Radolf,J.D.  
TITLE Evidence for in vivo but not in vitro expression of a Borrelia  
burgdorferi outer surface protein F (OspF) homologue  
JOURNAL Mol. Microbiol. 18 (3), 507-520 (1995)  
MEDLINE 96342380  
PubMed 8748034  
REFERENCE 2 (bases 1 to 3231)  
AUTHORS Akins,D.R.  
TITLE Direct Submission

JOURNAL Submitted (29-JUN-1995) Darrin R. Akins, UT Southwestern Med.  
School at Dallas, Molecular Microbiology, 5323 Harry Hines Blvd.,  
Dallas, TX 75235-9048, USA  
REFERENCE 3 (bases 1 to 3231)  
AUTHORS Akins,D.R.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUL-1998) Darrin R. Akins, UT Southwestern Med.  
School at Dallas, Molecular Microbiology, 5323 Harry Hines Blvd.,  
Dallas, TX 75235-9048, USA  
REMARK Sequence update by submitter  
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ORIGIN

Query Match 35.2%; Score 875.6; DB 1; Length 4283;  
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[illegible]

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DEFINITION	Borrelia burgdorferi B31 plasmid cp32-6, complete plasmid sequence.
ACCESSION	AE001578
VERSION	AE001578.1 GI:6382214
KEYWORDS	
SOURCE	Borrelia burgdorferi B31
ORGANISM	Borrelia burgdorferi B31
REFERENCE	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group.
AUTHORS	1 (bases 1 to 29838) Casjens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B., Rosa,P., Lathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Haft,D., Hickey,E., Winn,M., White,O. and Fraser,C.M. A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi Mol. Microbiol. 35 (3), 490-516 (2000)
JOURNAL	20138354
PUBMED	10672174
REFERENCE	2 (bases 1 to 29838) Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R., White,O., Dodson,R., Hickey,E.K., Winn,M., Peterson,J., van-Vugt,R., Palmer,N., Haft,D., Rosa,P. and Stevenson,B. Direct Submission Submitted (11-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
TITLE	Location/Qualifiers
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DEFINITION	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA)		
ACCESSION	Genes, complete cds; and unknown genes.		
VERSION	U42598		
KEYWORDS	U42598.1 GI:3559778		
SOURCE	Borrelia burgdorferi (Lyme disease spirochete)		
ORGANISM	Borrelia burgdorferi		
REFERENCE	Bacteria, Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;		
AUTHORS	Borrelia burgdorferi group.		
TITLE	1 (bases 1 to 3904) Stevenson,B., Tilly,K. and Rosa,P.A. A family of genes located on four separate 32-kilobase circular plasmids in Borrelia burgdorferi B31 J. Bacteriol. 178 (12), 3508-3516 (1996)		
JOURNAL	96256604		
MEDLINE	8655548		
PUBMED			
REFERENCE	2 (bases 1 to 3804) Stevenson,B., Tilly,K. and Rosa,P.A. Direct Submission		
AUTHORS	Submitted (08-DEC-1995) Brian Stevenson, Rocky Mountain Labs,		
TITLE	NIAD, NIH, 903 South 4th St., Hamilton, MT 59840, USA		
JOURNAL	3 (bases 1 to 3904) Stevenson,B. Direct Submission		
AUTHORS	Submitted (09-SEP-1998) Microbiology & Immunology, Univ. Kentucky,		
TITLE	800 Rose St., Lexington, KY 40536, USA		
REMARK	Sequence update by submitter		
COMMENT	On Sep 9, 1998 this sequence version replaced gi:1373114.		
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2656 CAAGCAAAAGATGGTGGTCAACAGAAAGAAAGAAAGAAAGAAAGAAATTTCAAGAA 2715

CDS

1320 GAAATGATAAGCTGTCTTTTATAGAGAGAGATCAAAAGAGG-----ATGAA 1367  
2716 TTAAGAGTAAATAGATAAAGAAAAAAGAAATTTAGAGAGGCTTAGAAGAAATTTCAA 2775

gene

1368 GAAGAAAAATGACCAAGCTGTTAATTTAGAAAGAAAAAATTTGCGGAAGAGAGTAAGAAAGTT 1427  
2776 GAAATTAAGAACAGATTTGAATCTGCAACTGGAGAAAGTACTGAGAAAGTTAAAAACAA 2835

CDS

1428 GTTAATTTAGAGAGAAAGATTTAGAGTATAAAGAGAGAGCTGAAGAGAGATGAAGATAA 1487  
2836 GGAATATTTGGCAAAAAAGCTTTTAAAGATATGCTAAAGAAATTTGGGTGTAAATGGAAGTTAT 2895

gene

1488 GAAGAAATAGAGAAAAACAAAAACAGAAAGTGGAAAAAGCACAAGAAAAACCAACGACAA 1547

Db	2896	TCTCTTAATGATGCTACTAATFACTAATGATTTTCTTAAAGGTTATAGATGATGCTCTT	2955
Qy	1548	GAAGAAAGAAACGAAAGAAACAGAGACAGAGAGAAAGAAACGAAACGACAGAA	1607
Db	2956	AAAAATATTGGAGAGAACTTTGAAAGCTAGCAGGCTCAAAATATAGAGATAAAAA	3015
Qy	1608	CAAGAAAGAAAGAGAGAGCTAAACAAATTAAGAACTTCGGATAAATAGATGAG	1667
Db	3016	TAATAAAAAATGGGTTTGTAGTAAAAATTAACACACAGACTAACCAATCAGTCTTA	3075
Qy	1668	ATAAGTTGGATATTGATGTATAGAAAGTCACACAGTGTAAACCGAAAGCAGTTATA	1727
Db	3076	TTGTTTATTAGCAATTTACATTCGTGAAATTTAGGCAA---TAAAGCTAGAGGGGATATG	3132
Qy	1728	GATAAATTTACGGGCTGTATATGATTTATTTACCGATGACACAAAGAAAGCTATATAT	1787
Db	3133	AAAAAATTAGTCTGTAAATTTTGTGTTTT-----ATTGTAGTA	3174
Qy	1788	AAACATGGGAGATTTTAGAAGATGAAGAGCGAGGATGGGAAATTTATTGAAAGAA	1847
Db	3175	AGTTTAAAGTCAAAATATAGAGAAATTTATACAGAACTAAAGAGCTTTTCTTAAAGAA	3234
Qy	1848	TTGATGATACCTAGAGATGAGTTAAGAACCAATTAATTAAGATATTAATAATTTAT	1907
Db	3235	GATTTTAACTTAATAATAAGACTAGATAATTATGATTTTAAATGAGTATGAAAA	3294
Qy	1908	GCCATGAAATGAGCCTCCTCTAAAGAAATGTAGATGTCAGCGAAATTAAGAGAT	1967
Db	3295	AGTCATGTTTTTCCGATGCTCCTAGAAATTAGAGGAGATTAAAGAAAAATGGAATTAAA	3354
Qy	1968	TTAGAAAGTAAATCAGGATTAGAAAGTTAAAGATATCTTAAAGCAATTTCTATA	2027
Db	3355	GAAAAAGTGTTTTTTTGGAGCTCTTGAGGCTATTGATATCTTATAAAATTAAGATA	3414
Qy	2028	TTTGAGAAATTA	2040
Db	3415	AGTACTGATAGTA	3427

Search completed: July 29, 2004, 19:12:40  
Job time : 9607 secs